

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 15:17:59 ; Search time 1605 Seconds  
(without alignments)  
294.640 Million cell updates/sec

Title: US-09-813-824A-3  
Perfect score: 10  
Sequence: 1 RRRCCWGGYY 10

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2172512

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	6 A67159	A67159 Sequence 16
2	10	100.0	10	6 A67159	A67159 Sequence 16
3	10	100.0	10	6 AR003507	AR003507 Sequence
4	10	100.0	10	6 AR003507	AR003507 Sequence
5	10	100.0	10	6 AR070749	AR070749 Sequence
6	10	100.0	10	6 AR070749	AR070749 Sequence
7	10	100.0	10	6 AR074547	AR074547 Sequence
8	10	100.0	10	6 AR074547	AR074547 Sequence
9	10	100.0	10	6 AR124219	AR124219 Sequence
10	10	100.0	10	6 AR124219	AR124219 Sequence
11	10	100.0	10	6 AR157427	AR157427 Sequence
12	10	100.0	10	6 AR157427	AR157427 Sequence
13	10	100.0	10	6 I62424	I62424 Sequence 30
14	10	100.0	10	6 I62424	I62424 Sequence 30
15	10	100.0	10	6 AR303877	AR303877 Sequence
16	10	100.0	10	6 AR303877	AR303877 Sequence
17	10	100.0	10	6 AX077262	AX077262 Sequence
18	10	100.0	10	6 AX077262	AX077262 Sequence
19	10	100.0	10	6 AX339211	AX339211 Sequence

c 20	10	100.0	10	6 AX339211	AX339211 Sequence
c 21	10	100.0	10	6 AX776278	AX776278 Sequence
c 22	10	100.0	10	6 AX776278	AX776278 Sequence
c 23	10	100.0	10	6 AX803572	AX803572 Sequence
c 24	10	100.0	10	6 AX803572	AX803572 Sequence
c 25	10	100.0	10	6 BD064950	BD064950 Method fo
c 26	10	100.0	10	6 BD064950	BD064950 Method fo
c 27	10	100.0	10	6 BD084759	BD084759 Human ner
c 28	10	100.0	10	6 BD084759	BD084759 Human ner
c 29	10	100.0	19	6 AX685336	AX685336 Sequence
c 30	10	100.0	19	6 AX685336	AX685336 Sequence
c 31	10	100.0	20	6 AR181179	AR181179 Sequence
c 32	10	100.0	20	6 AR181179	AR181179 Sequence
c 33	10	100.0	21	6 AR060431	AR060431 Sequence
c 34	10	100.0	21	6 AR060431	AR060431 Sequence
c 35	5	50.0	20	6 I22646	I22646 Sequence 13
c 36	5	50.0	20	6 I22646	I22646 Sequence 13
c 37	5	50.0	20	6 I47471	I47471 Sequence 13
c 38	5	50.0	20	6 I47471	I47471 Sequence 13
c 39	4	40.0	10	6 CQ771564	CQ771564 Sequence
c 40	4	40.0	10	6 CQ771564	CQ771564 Sequence
c 41	4	40.0	10	6 I74680	I74680 Sequence 9
c 42	4	40.0	10	6 I74680	I74680 Sequence 9
c 43	4	40.0	10	6 I91766	I91766 Sequence 9
c 44	4	40.0	10	6 I91766	I91766 Sequence 9
c 45	4	40.0	10	6 BD090936	BD090936 Method fo
c 46	4	40.0	10	6 BD090936	BD090936 Method fo
c 47	4	40.0	12	6 BD084901	BD084901 Character
c 48	4	40.0	12	6 BD084901	BD084901 Character
c 49	4	40.0	19	6 AR451567	AR451567 Sequence
c 50	4	40.0	19	6 AR451567	AR451567 Sequence
c 51	4	40.0	19	6 AX412112	AX412112 Sequence
c 52	4	40.0	19	6 AX412112	AX412112 Sequence
c 53	4	40.0	20	6 BD184677	BD184677 Method an
c 54	4	40.0	20	6 BD184677	BD184677 Method an
c 55	4	40.0	20	6 I22645	I22645 Sequence 13
c 56	4	40.0	20	6 I22645	I22645 Sequence 13
c 57	4	40.0	20	6 I22647	I22647 Sequence 13
c 58	4	40.0	20	6 I22647	I22647 Sequence 13
c 59	4	40.0	20	6 I47470	I47470 Sequence 13
c 60	4	40.0	20	6 I47470	I47470 Sequence 13
c 61	4	40.0	20	6 I47472	I47472 Sequence 13
c 62	4	40.0	20	6 I47472	I47472 Sequence 13
c 63	4	40.0	27	6 AR030183	AR030183 Sequence
c 64	4	40.0	27	6 AR030183	AR030183 Sequence
c 65	4	40.0	27	6 AR030187	AR030187 Sequence
c 66	4	40.0	27	6 AR030187	AR030187 Sequence
c 67	4	40.0	27	6 AR140600	AR140600 Sequence
c 68	4	40.0	27	6 AR140600	AR140600 Sequence
c 69	4	40.0	27	6 I17358	I17358 Sequence 8
c 70	4	40.0	27	6 I17358	I17358 Sequence 8
c 71	4	40.0	27	6 I17359	I17359 Sequence 9
c 72	4	40.0	27	6 I17359	I17359 Sequence 9
c 73	4	40.0	27	6 AR477281	AR477281 Sequence
c 74	4	40.0	27	6 AR477281	AR477281 Sequence
c 75	4	40.0	27	6 AR477282	AR477282 Sequence
c 76	4	40.0	27	6 AR477282	AR477282 Sequence
c 77	4	40.0	38	6 BD132388	BD132388 DNA diagn
c 78	4	40.0	38	6 BD132388	BD132388 DNA diagn
c 79	4	40.0	42	6 AX328823	AX328823 Sequence
c 80	4	40.0	42	6 AX328823	AX328823 Sequence
c 81	4	40.0	63	4 DOGS7SL1	M30845 Dog signal
c 82	4	40.0	63	4 DOGS7SL1	M30845 Dog signal
c 83	3	30.0	6	6 A90866	A90866 Sequence 1
c 84	3	30.0	6	6 A90866	A90866 Sequence 1
c 85	3	30.0	6	6 E64767	E64767 Chemically
c 86	3	30.0	6	6 E64767	E64767 Chemically
c 87	3	30.0	6	6 AX797664	AX797664 Sequence
c 88	3	30.0	6	6 AX797664	AX797664 Sequence
c 89	3	30.0	6	6 AX957648	AX957648 Sequence
c 90	3	30.0	6	6 AX957648	AX957648 Sequence
c 91	3	30.0	6	6 AX957742	AX957742 Sequence
c 92	3	30.0	6	6 AX957742	AX957742 Sequence

c 93	3	30.0	6	6	AX958147	AX958147 Sequence	c 166	3	30.0	11	6	AX012240	AX012240 Sequence
c 94	3	30.0	6	6	AX958147	AX958147 Sequence	c 167	3	30.0	11	6	AX711145	AX711145 Sequence
c 95	3	30.0	7	6	BD211369	BD211369 Method of	c 168	3	30.0	11	6	AX711145	AX711145 Sequence
c 96	3	30.0	7	6	BD211369	BD211369 Method of	c 169	3	30.0	11	6	AX711146	AX711146 Sequence
c 97	3	30.0	7	6	BD211370	BD211370 Method of	c 170	3	30.0	11	6	AX711146	AX711146 Sequence
c 98	3	30.0	7	6	BD211370	BD211370 Method of	c 171	3	30.0	11	6	AX711147	AX711147 Sequence
c 99	3	30.0	8	6	E64766	E64766 Chemically	c 172	3	30.0	11	6	AX711147	AX711147 Sequence
c 100	3	30.0	8	6	E64766	E64766 Chemically	c 173	3	30.0	11	6	AX711148	AX711148 Sequence
c 101	3	30.0	8	6	AX046162	AX046162 Sequence	c 174	3	30.0	11	6	AX711148	AX711148 Sequence
c 102	3	30.0	8	6	AX046162	AX046162 Sequence	c 175	3	30.0	12	6	I84596	I84596 Sequence 2
c 103	3	30.0	8	6	BD084758	BD084758 Human ner	c 176	3	30.0	12	6	I84596	I84596 Sequence 2
c 104	3	30.0	8	6	BD084758	BD084758 Human ner	c 177	3	30.0	12	6	I84608	I84608 Sequence 14
c 105	3	30.0	10	6	A37861	A37861 Sequence 4	c 178	3	30.0	12	6	I84608	I84608 Sequence 14
c 106	3	30.0	10	6	A37861	A37861 Sequence 4	c 179	3	30.0	12	6	AX412933	AX412933 Sequence
c 107	3	30.0	10	6	AR074451	AR074451 Sequence	c 180	3	30.0	12	6	AX412933	AX412933 Sequence
c 108	3	30.0	10	6	AR074451	AR074451 Sequence	c 181	3	30.0	12	6	AX816374	AX816374 Sequence
c 109	3	30.0	10	6	AR081131	AR081131 Sequence	c 182	3	30.0	12	6	AX816374	AX816374 Sequence
c 110	3	30.0	10	6	AR081131	AR081131 Sequence	c 183	3	30.0	12	6	AX816375	AX816375 Sequence
c 111	3	30.0	10	6	AR085328	AR085328 Sequence	c 184	3	30.0	12	6	AX816375	AX816375 Sequence
c 112	3	30.0	10	6	AR085328	AR085328 Sequence	c 185	3	30.0	12	6	BD074027	BD074027 Human g11
c 113	3	30.0	10	6	AR088076	AR088076 Sequence	c 186	3	30.0	12	6	BD074027	BD074027 Human g11
c 114	3	30.0	10	6	AR088076	AR088076 Sequence	c 187	3	30.0	13	6	I27012	I27012 Sequence 33
c 115	3	30.0	10	6	AR104235	AR104235 Sequence	c 188	3	30.0	13	6	I27012	I27012 Sequence 33
c 116	3	30.0	10	6	AR104235	AR104235 Sequence	c 189	3	30.0	13	6	I84597	I84597 Sequence 3
c 117	3	30.0	10	6	AR110243	AR110243 Sequence	c 190	3	30.0	13	6	I84597	I84597 Sequence 3
c 118	3	30.0	10	6	AR110243	AR110243 Sequence	c 191	3	30.0	13	6	I84609	I84609 Sequence 15
c 119	3	30.0	10	6	AR134895	AR134895 Sequence	c 192	3	30.0	13	6	I84609	I84609 Sequence 15
c 120	3	30.0	10	6	AR134895	AR134895 Sequence	c 193	3	30.0	13	6	AX235305	AX235305 Sequence
c 121	3	30.0	10	6	AR139421	AR139421 Sequence	c 194	3	30.0	13	6	AX235305	AX235305 Sequence
c 122	3	30.0	10	6	AR139421	AR139421 Sequence	c 195	3	30.0	14	6	AR134892	AR134892 Sequence
c 123	3	30.0	10	6	AR143499	AR143499 Sequence	c 196	3	30.0	14	6	AR134892	AR134892 Sequence
c 124	3	30.0	10	6	AR143499	AR143499 Sequence	c 197	3	30.0	14	6	AR138914	AR138914 Sequence
c 125	3	30.0	10	6	AR170002	AR170002 Sequence	c 198	3	30.0	14	6	AR138914	AR138914 Sequence
c 126	3	30.0	10	6	AR170002	AR170002 Sequence	c 199	3	30.0	14	6	AR156467	AR156467 Sequence
c 127	3	30.0	10	6	AR171403	AR171403 Sequence	c 200	3	30.0	14	6	AR156467	AR156467 Sequence
c 128	3	30.0	10	6	AR171403	AR171403 Sequence	c 201	3	30.0	14	6	BD211484	BD211484 Modifying
c 129	3	30.0	10	6	AR171574	AR171574 Sequence	c 202	3	30.0	14	6	BD211484	BD211484 Modifying
c 130	3	30.0	10	6	AR171574	AR171574 Sequence	c 203	3	30.0	14	6	BD221627	BD221627 Upstream
c 131	3	30.0	10	6	AR171811	AR171811 Sequence	c 204	3	30.0	14	6	BD221627	BD221627 Upstream
c 132	3	30.0	10	6	AR171811	AR171811 Sequence	c 205	3	30.0	14	6	BD222103	BD222103 Upstream
c 133	3	30.0	10	6	BD189505	BD189505 PROMOTER	c 206	3	30.0	14	6	BD222103	BD222103 Upstream
c 134	3	30.0	10	6	BD189505	BD189505 PROMOTER	c 207	3	30.0	14	6	I38794	I38794 Sequence 32
c 135	3	30.0	10	6	BD243164	BD243164 MN gene a	c 208	3	30.0	14	6	I38794	I38794 Sequence 32
c 136	3	30.0	10	6	BD243164	BD243164 MN gene a	c 209	3	30.0	14	6	I84598	I84598 Sequence 4
c 137	3	30.0	10	6	CQ814515	CQ814515 Sequence	c 210	3	30.0	14	6	I84598	I84598 Sequence 4
c 138	3	30.0	10	6	CQ814515	CQ814515 Sequence	c 211	3	30.0	14	6	I84610	I84610 Sequence 16
c 139	3	30.0	10	6	I72403	I72403 Sequence 34	c 212	3	30.0	14	6	I84610	I84610 Sequence 16
c 140	3	30.0	10	6	I72403	I72403 Sequence 34	c 213	3	30.0	14	6	AR287313	AR287313 Sequence
c 141	3	30.0	10	6	I84595	I84595 Sequence 1	c 214	3	30.0	14	6	AR287313	AR287313 Sequence
c 142	3	30.0	10	6	I84595	I84595 Sequence 1	c 215	3	30.0	14	6	AR339730	AR339730 Sequence
c 143	3	30.0	10	6	I84606	I84606 Sequence 12	c 216	3	30.0	14	6	AR339730	AR339730 Sequence
c 144	3	30.0	10	6	I84606	I84606 Sequence 12	c 217	3	30.0	14	6	AX711201	AX711201 Sequence
c 145	3	30.0	10	6	AR220243	AR220243 Sequence	c 218	3	30.0	14	6	AX711201	AX711201 Sequence
c 146	3	30.0	10	6	AR220243	AR220243 Sequence	c 219	3	30.0	14	6	BD174481	BD174481 DNA part1
c 147	3	30.0	10	6	AR264148	AR264148 Sequence	c 220	3	30.0	14	6	BD174481	BD174481 DNA part1
c 148	3	30.0	10	6	AR264148	AR264148 Sequence	c 221	3	30.0	15	6	AR076616	AR076616 Sequence
c 149	3	30.0	10	6	AR362282	AR362282 Sequence	c 222	3	30.0	15	6	AR076616	AR076616 Sequence
c 150	3	30.0	10	6	AR362282	AR362282 Sequence	c 223	3	30.0	15	6	AR094365	AR094365 Sequence
c 151	3	30.0	10	6	AX412946	AX412946 Sequence	c 224	3	30.0	15	6	AR094365	AR094365 Sequence
c 152	3	30.0	10	6	AX412946	AX412946 Sequence	c 225	3	30.0	15	6	I84599	I84599 Sequence 5
c 153	3	30.0	10	6	AX497559	AX497559 Sequence	c 226	3	30.0	15	6	I84599	I84599 Sequence 5
c 154	3	30.0	10	6	AX497559	AX497559 Sequence	c 227	3	30.0	15	6	I84611	I84611 Sequence 17
c 155	3	30.0	10	6	BD009036	BD009036 Promoter	c 228	3	30.0	15	6	I84611	I84611 Sequence 17
c 156	3	30.0	10	6	BD009036	BD009036 Promoter	c 229	3	30.0	15	6	AR399667	AR399667 Sequence
c 157	3	30.0	10	6	BD063695	BD063695 Glutathio	c 230	3	30.0	15	6	AR399667	AR399667 Sequence
c 158	3	30.0	10	6	BD063695	BD063695 Glutathio	c 231	3	30.0	15	6	AR477239	AR477239 Sequence
c 159	3	30.0	10	6	BD073429	BD073429 Expressio	c 232	3	30.0	15	6	AR477239	AR477239 Sequence
c 160	3	30.0	10	6	BD073429	BD073429 Expressio	c 233	3	30.0	16	6	AR010020	AR010020 Sequence
c 161	3	30.0	10	6	BD091328	BD091328 In vitro	c 234	3	30.0	16	6	AR010020	AR010020 Sequence
c 162	3	30.0	10	6	BD091328	BD091328 In vitro	c 235	3	30.0	16	6	AR034755	AR034755 Sequence
c 163	3	30.0	11	6	I84607	I84607 Sequence 13	c 236	3	30.0	16	6	AR034755	AR034755 Sequence
c 164	3	30.0	11	6	I84607	I84607 Sequence 13	c 237	3	30.0	16	6	BD272242	BD272242 Anti-angi
c 165	3	30.0	11	6	AX012240	AX012240 Sequence	c 238	3	30.0	16	6	BD272242	BD272242 Anti-angi



C 385	3	30.0	21	6	A07255	A07255 Oligonucleo	C 458	3	30.0	24	6	E47132	E47132 Protein fro
C 386	3	30.0	21	6	A07255	A07255 Oligonucleo	C 459	3	30.0	24	6	AR300918	AR300918 Sequence
C 387	3	30.0	21	6	AR169411	AR169411 Sequence	C 460	3	30.0	24	6	AR300918	AR300918 Sequence
C 388	3	30.0	21	6	AR169411	AR169411 Sequence	C 461	3	30.0	24	6	AR490304	AR490304 Sequence
C 389	3	30.0	21	6	AR169413	AR169413 Sequence	C 462	3	30.0	24	6	AR490304	AR490304 Sequence
C 390	3	30.0	21	6	AR169413	AR169413 Sequence	C 463	3	30.0	24	6	AX019962	AX019962 Sequence
C 391	3	30.0	21	6	AR169442	AR169442 Sequence	C 464	3	30.0	24	6	AX019962	AX019962 Sequence
C 392	3	30.0	21	6	AR169442	AR169442 Sequence	C 465	3	30.0	24	6	AR030182	AR030182 Sequence
C 393	3	30.0	21	6	AR169444	AR169444 Sequence	C 466	3	30.0	25	6	AR030182	AR030182 Sequence
C 394	3	30.0	21	6	AR169444	AR169444 Sequence	C 467	3	30.0	25	6	AR065198	AR065198 Sequence
C 395	3	30.0	21	6	BD231011	BD231011 Mammalian	C 468	3	30.0	25	6	AR065198	AR065198 Sequence
C 396	3	30.0	21	6	BD231011	BD231011 Mammalian	C 469	3	30.0	25	6	I17357	I17357 Sequence 7
C 397	3	30.0	21	6	I22810	I22810 Sequence 29	C 470	3	30.0	25	6	I17357	I17357 Sequence 7
C 398	3	30.0	21	6	I22810	I22810 Sequence 29	C 471	3	30.0	25	6	AR322479	AR322479 Sequence
C 399	3	30.0	21	6	I47635	I47635 Sequence 29	C 472	3	30.0	25	6	AR322479	AR322479 Sequence
C 400	3	30.0	21	6	I47635	I47635 Sequence 29	C 473	3	30.0	25	6	AR477280	AR477280 Sequence
C 401	3	30.0	21	6	AX711231	AX711231 Sequence	C 474	3	30.0	25	6	AR477280	AR477280 Sequence
C 402	3	30.0	21	6	AX711231	AX711231 Sequence	C 475	3	30.0	25	6	AX300979	AX300979 Sequence
C 403	3	30.0	21	6	AX774486	AX774486 Sequence	C 476	3	30.0	25	6	AX300979	AX300979 Sequence
C 404	3	30.0	21	6	AX774486	AX774486 Sequence	C 477	3	30.0	25	6	AX300995	AX300995 Sequence
C 405	3	30.0	21	6	AX955618	AX955618 Sequence	C 478	3	30.0	25	6	AX300995	AX300995 Sequence
C 406	3	30.0	21	6	AX955618	AX955618 Sequence	C 479	3	30.0	25	6	BD003196	BD003196 HPPD gene
C 407	3	30.0	21	6	BD085429	BD085429 Method fo	C 480	3	30.0	25	6	BD003196	BD003196 HPPD gene
C 408	3	30.0	21	6	BD085429	BD085429 Method fo	C 481	3	30.0	25	6	BD003199	BD003199 HPPD gene
C 409	3	30.0	21	6	BD085435	BD085435 Method fo	C 482	3	30.0	25	6	BD003199	BD003199 HPPD gene
C 410	3	30.0	21	6	BD085435	BD085435 Method fo	C 483	3	30.0	26	6	A23804	A23804 Artificial
C 411	3	30.0	22	6	A65929	A65929 Sequence 5	C 484	3	30.0	26	6	A23804	A23804 Artificial
C 412	3	30.0	22	6	A65929	A65929 Sequence 5	C 485	3	30.0	26	6	AR061661	AR061661 Sequence
C 413	3	30.0	22	6	AR168703	AR168703 Sequence	C 486	3	30.0	26	6	AR061661	AR061661 Sequence
C 414	3	30.0	22	6	AR168703	AR168703 Sequence	C 487	3	30.0	26	6	AR108560	AR108560 Sequence
C 415	3	30.0	22	6	AX003361	AX003361 Sequence	C 488	3	30.0	26	6	AR108560	AR108560 Sequence
C 416	3	30.0	22	6	AX003361	AX003361 Sequence	C 489	3	30.0	26	6	AR140606	AR140606 Sequence
C 417	3	30.0	23	6	A19190	A19190 Markush oli	C 490	3	30.0	26	6	AR140606	AR140606 Sequence
C 418	3	30.0	23	6	A19190	A19190 Markush oli	C 491	3	30.0	26	6	AR140991	AR140991 Sequence
C 419	3	30.0	23	6	AR032167	AR032167 Sequence	C 492	3	30.0	26	6	AR140991	AR140991 Sequence
C 420	3	30.0	23	6	AR032167	AR032167 Sequence	C 493	3	30.0	26	6	I16517	I16517 Sequence 34
C 421	3	30.0	23	6	AR145983	AR145983 Sequence	C 494	3	30.0	26	6	I16517	I16517 Sequence 34
C 422	3	30.0	23	6	AR145983	AR145983 Sequence	C 495	3	30.0	26	6	I17360	I17360 Sequence 10
C 423	3	30.0	23	6	AR169397	AR169397 Sequence	C 496	3	30.0	26	6	I17360	I17360 Sequence 10
C 424	3	30.0	23	6	AR169397	AR169397 Sequence	C 497	3	30.0	26	6	I67003	I67003 Sequence 34
C 425	3	30.0	23	6	AR169399	AR169399 Sequence	C 498	3	30.0	26	6	I67003	I67003 Sequence 34
C 426	3	30.0	23	6	AR169399	AR169399 Sequence	C 499	3	30.0	26	6	I85097	I85097 Sequence 34
C 427	3	30.0	23	6	BD188516	BD188516 Method fo	C 500	3	30.0	26	6	I85097	I85097 Sequence 34
C 428	3	30.0	23	6	BD188516	BD188516 Method fo	C 501	3	30.0	26	6	AR263521	AR263521 Sequence
C 429	3	30.0	23	6	CQ778460	CQ778460 Sequence	C 502	3	30.0	26	6	AR263521	AR263521 Sequence
C 430	3	30.0	23	6	CQ778460	CQ778460 Sequence	C 503	3	30.0	26	6	AR477283	AR477283 Sequence
C 431	3	30.0	23	6	E51219	E51219 Disease tol	C 504	3	30.0	26	6	AR477283	AR477283 Sequence
C 432	3	30.0	23	6	E51219	E51219 Disease tol	C 505	3	30.0	26	6	AX109901	AX109901 Sequence
C 433	3	30.0	23	6	AR180874	AR180874 Sequence	C 506	3	30.0	26	6	AX109901	AX109901 Sequence
C 434	3	30.0	23	6	AR180874	AR180874 Sequence	C 507	3	30.0	26	6	AX363332	AX363332 Sequence
C 435	3	30.0	23	6	AX181866	AX181866 Sequence	C 508	3	30.0	26	6	AX363332	AX363332 Sequence
C 436	3	30.0	23	6	AX181866	AX181866 Sequence	C 509	3	30.0	26	6	AX443035	AX443035 Sequence
C 437	3	30.0	23	6	AX181973	AX181973 Sequence	C 510	3	30.0	26	6	AX443035	AX443035 Sequence
C 438	3	30.0	23	6	AX181973	AX181973 Sequence	C 511	3	30.0	26	6	AX443036	AX443036 Sequence
C 439	3	30.0	23	6	AX250634	AX250634 Sequence	C 512	3	30.0	26	6	AX443036	AX443036 Sequence
C 440	3	30.0	23	6	AX250634	AX250634 Sequence	C 513	3	30.0	26	6	BD080417	BD080417 Direct qu
C 441	3	30.0	23	6	AX392031	AX392031 Sequence	C 514	3	30.0	26	6	BD080417	BD080417 Direct qu
C 442	3	30.0	23	6	AX392031	AX392031 Sequence	C 515	3	30.0	27	6	AR061655	AR061655 Sequence
C 443	3	30.0	23	6	BD077266	BD077266 Method an	C 516	3	30.0	27	6	AR061655	AR061655 Sequence
C 444	3	30.0	23	6	BD077266	BD077266 Method an	C 517	3	30.0	27	6	AR108554	AR108554 Sequence
C 445	3	30.0	23	6	BD103211	BD103211 Factors i	C 518	3	30.0	27	6	AR108554	AR108554 Sequence
C 446	3	30.0	23	6	BD103211	BD103211 Factors i	C 519	3	30.0	27	6	AR117011	AR117011 Sequence
C 447	3	30.0	23	6	BD144117	BD144117 DNA marke	C 520	3	30.0	27	6	AR117011	AR117011 Sequence
C 448	3	30.0	23	6	BD144117	BD144117 DNA marke	C 521	3	30.0	27	6	AR140599	AR140599 Sequence
C 449	3	30.0	24	6	A32253	A32253 Synthetic M	C 522	3	30.0	27	6	AR140599	AR140599 Sequence
C 450	3	30.0	24	6	A32253	A32253 Synthetic M	C 523	3	30.0	27	6	AR140990	AR140990 Sequence
C 451	3	30.0	24	6	AR109608	AR109608 Sequence	C 524	3	30.0	27	6	AR140990	AR140990 Sequence
C 452	3	30.0	24	6	AR109608	AR109608 Sequence	C 525	3	30.0	27	6	BD195163	BD195163 CXCR3 che
C 453	3	30.0	24	6	AR109806	AR109806 Sequence	C 526	3	30.0	27	6	BD195163	BD195163 CXCR3 che
C 454	3	30.0	24	6	AR109806	AR109806 Sequence	C 527	3	30.0	27	6	E38902	E38902 Chimeric an
C 455	3	30.0	24	6	E12479	E12479 PCR primer	C 528	3	30.0	27	6	E38902	E38902 Chimeric an
C 456	3	30.0	24	6	E12479	E12479 PCR primer	C 529	3	30.0	27	6	I16511	I16511 Sequence 33
C 457	3	30.0	24	6	E47132	E47132 Protein fro	C 530	3	30.0	27	6	I16511	I16511 Sequence 33



c 531	3	30.0	27	6	I66997	I66997 Sequence 33	c 604	3	30.0	33	6	AR004374	Sequence
c 532	3	30.0	27	6	I66997	I66997 Sequence 33	c 605	3	30.0	33	6	AR004384	Sequence
c 533	3	30.0	27	6	I85091	I85091 Sequence 33	c 606	3	30.0	33	6	AR004384	Sequence
c 534	3	30.0	27	6	I85091	I85091 Sequence 33	c 607	3	30.0	33	6	AR097143	Sequence
c 535	3	30.0	27	6	AR263515	AR263515 Sequence	c 608	3	30.0	33	6	AR097143	Sequence
c 536	3	30.0	27	6	AR263515	AR263515 Sequence	c 609	3	30.0	33	6	AR097162	Sequence
c 537	3	30.0	27	6	AR409564	AR409564 Sequence	c 610	3	30.0	33	6	AR097162	Sequence
c 538	3	30.0	27	6	AR409564	AR409564 Sequence	c 611	3	30.0	33	6	AR097165	Sequence
c 539	3	30.0	27	6	AR443097	AR443097 Sequence	c 612	3	30.0	33	6	AR097165	Sequence
c 540	3	30.0	27	6	AR443097	AR443097 Sequence	c 613	3	30.0	33	6	AR097175	Sequence
c 541	3	30.0	27	6	AR456182	AR456182 Sequence	c 614	3	30.0	33	6	AR097175	Sequence
c 542	3	30.0	27	6	AR456182	AR456182 Sequence	c 615	3	30.0	33	6	AR104485	Sequence
c 543	3	30.0	27	6	AR068016	AR068016 Sequence	c 616	3	30.0	33	6	AR104485	Sequence
c 544	3	30.0	27	6	AR068016	AR068016 Sequence	c 617	3	30.0	33	6	AR130641	Sequence
c 545	3	30.0	28	6	AX278295	AX278295 Sequence	c 618	3	30.0	33	6	AR130641	Sequence
c 546	3	30.0	28	6	AX278295	AX278295 Sequence	c 619	3	30.0	33	6	AR130660	Sequence
c 547	3	30.0	28	6	AX428390	AX428390 Sequence	c 620	3	30.0	33	6	AR130660	Sequence
c 548	3	30.0	28	6	AX428390	AX428390 Sequence	c 621	3	30.0	33	6	AR130663	Sequence
c 549	3	30.0	28	6	AX823605	AX823605 Sequence	c 622	3	30.0	33	6	AR130663	Sequence
c 550	3	30.0	28	6	AX823605	AX823605 Sequence	c 623	3	30.0	33	6	AR130673	Sequence
c 551	3	30.0	29	6	AR061660	AR061660 Sequence	c 624	3	30.0	33	6	AR130673	Sequence
c 552	3	30.0	29	6	AR061660	AR061660 Sequence	c 625	3	30.0	33	6	AR147201	Sequence
c 553	3	30.0	29	6	AR108559	AR108559 Sequence	c 626	3	30.0	33	6	AR147201	Sequence
c 554	3	30.0	29	6	AR108559	AR108559 Sequence	c 627	3	30.0	33	6	AR147201	Sequence
c 555	3	30.0	29	6	CQ813531	CQ813531 Sequence	c 628	3	30.0	33	6	AR171990	Sequence
c 556	3	30.0	29	6	CQ813531	CQ813531 Sequence	c 629	3	30.0	33	6	AR171990	Sequence
c 557	3	30.0	29	6	I16516	I16516 Sequence 34	c 630	3	30.0	33	6	AR172009	Sequence
c 558	3	30.0	29	6	I16516	I16516 Sequence 34	c 631	3	30.0	33	6	AR172012	Sequence
c 559	3	30.0	29	6	I17750	I17750 Sequence 25	c 632	3	30.0	33	6	AR172012	Sequence
c 560	3	30.0	29	6	I17750	I17750 Sequence 25	c 633	3	30.0	33	6	AR172022	Sequence
c 561	3	30.0	29	6	I67002	I67002 Sequence 34	c 634	3	30.0	33	6	AR172022	Sequence
c 562	3	30.0	29	6	I67002	I67002 Sequence 34	c 635	3	30.0	33	6	AR172022	Sequence
c 563	3	30.0	29	6	I85096	I85096 Sequence 34	c 636	3	30.0	33	6	BD189107	HCV Genom
c 564	3	30.0	29	6	I85096	I85096 Sequence 34	c 637	3	30.0	33	6	BD189107	HCV Genom
c 565	3	30.0	29	6	AR213667	AR213667 Sequence	c 638	3	30.0	33	6	BD189126	HCV Genom
c 566	3	30.0	29	6	AR213667	AR213667 Sequence	c 639	3	30.0	33	6	BD189126	HCV Genom
c 567	3	30.0	29	6	AR263520	AR263520 Sequence	c 640	3	30.0	33	6	BD189129	HCV Genom
c 568	3	30.0	29	6	AR263520	AR263520 Sequence	c 641	3	30.0	33	6	BD189129	HCV Genom
c 569	3	30.0	29	6	BD057726	BD057726 Fusion pr	c 642	3	30.0	33	6	BD189139	HCV Genom
c 570	3	30.0	29	6	BD057726	BD057726 Fusion pr	c 643	3	30.0	33	6	BD189139	HCV Genom
c 571	3	30.0	29	6	BD081556	BD081556 Soluble s	c 644	3	30.0	33	6	BD189254	HCV Genom
c 572	3	30.0	29	6	BD081556	BD081556 Soluble s	c 645	3	30.0	33	6	BD189254	HCV Genom
c 573	3	30.0	30	6	AG2994	AG2994 Sequence 6	c 646	3	30.0	33	6	BD189273	HCV Genom
c 574	3	30.0	30	6	AG2994	AG2994 Sequence 6	c 647	3	30.0	33	6	BD189273	HCV Genom
c 575	3	30.0	30	6	AR000084	AR000084 Sequence	c 648	3	30.0	33	6	BD189276	HCV Genom
c 576	3	30.0	30	6	AR000084	AR000084 Sequence	c 649	3	30.0	33	6	BD189276	HCV Genom
c 577	3	30.0	30	6	AR064907	AR064907 Sequence	c 650	3	30.0	33	6	BD189286	HCV Genom
c 578	3	30.0	30	6	AR064907	AR064907 Sequence	c 651	3	30.0	33	6	BD189401	HCV Genom
c 579	3	30.0	30	6	BD184673	BD184673 Method an	c 652	3	30.0	33	6	BD189401	HCV Genom
c 580	3	30.0	30	6	BD184673	BD184673 Method an	c 653	3	30.0	33	6	BD189420	HCV Genom
c 581	3	30.0	30	6	AX190506	AX190506 Sequence	c 654	3	30.0	33	6	BD189420	HCV Genom
c 582	3	30.0	30	6	AX190506	AX190506 Sequence	c 655	3	30.0	33	6	BD189423	HCV Genom
c 583	3	30.0	30	6	BD091329	BD091329 In vitro	c 656	3	30.0	33	6	BD189423	HCV Genom
c 584	3	30.0	30	6	BD091329	BD091329 In vitro	c 657	3	30.0	33	6	BD189433	HCV Genom
c 585	3	30.0	30	6	BD095227	BD095227 Polypepti	c 658	3	30.0	33	6	BD189433	HCV Genom
c 586	3	30.0	30	6	BD095227	BD095227 Polypepti	c 659	3	30.0	33	6	I11453	Sequence 7
c 587	3	30.0	31	6	AR035919	AR035919 Sequence	c 660	3	30.0	33	6	I11453	Sequence 7
c 588	3	30.0	31	6	AR035919	AR035919 Sequence	c 661	3	30.0	33	6	I11457	Sequence 11
c 589	3	30.0	31	6	I20155	I20155 Sequence 11	c 662	3	30.0	33	6	I11457	Sequence 11
c 590	3	30.0	31	6	I20155	I20155 Sequence 11	c 663	3	30.0	33	6	I82827	Sequence 6
c 591	3	30.0	31	6	AR340333	AR340333 Sequence	c 664	3	30.0	33	6	I82827	Sequence 6
c 592	3	30.0	31	6	AR340333	AR340333 Sequence	c 665	3	30.0	33	6	I82846	Sequence 25
c 593	3	30.0	32	6	AX591060	AX591060 Sequence	c 666	3	30.0	33	6	I82846	Sequence 25
c 594	3	30.0	32	6	AX591060	AX591060 Sequence	c 667	3	30.0	33	6	I82849	Sequence 28
c 595	3	30.0	32	6	AX810857	AX810857 Sequence	c 668	3	30.0	33	6	I82849	Sequence 28
c 596	3	30.0	32	6	AX810857	AX810857 Sequence	c 669	3	30.0	33	6	I82859	Sequence 38
c 597	3	30.0	32	6	BD087264	BD087264 Hyaluroa	c 670	3	30.0	33	6	I82859	Sequence 38
c 598	3	30.0	32	6	BD087264	BD087264 Hyaluroa	c 671	3	30.0	33	6	AR202452	Sequence
c 599	3	30.0	33	6	AR004352	AR004352 Sequence	c 672	3	30.0	33	6	AR202452	Sequence
c 600	3	30.0	33	6	AR004352	AR004352 Sequence	c 673	3	30.0	33	6	AR368953	Sequence
c 601	3	30.0	33	6	AR004371	AR004371 Sequence	c 674	3	30.0	33	6	AR368953	Sequence
c 602	3	30.0	33	6	AR004371	AR004371 Sequence	c 675	3	30.0	33	6	AR368967	Sequence
c 603	3	30.0	33	6	AR004374	AR004374 Sequence	c 676	3	30.0	33	6	AR368967	Sequence

677	3	30.0	33	6	AR369007	AR369007 Sequence	c 750	3	30.0	45	6	AR145060	AR145060 Sequence
c 678	3	30.0	33	6	AR369007	AR369007 Sequence	c 751	3	30.0	45	6	AR145061	AR145061 Sequence
679	3	30.0	33	6	AX190505	AX190505 Sequence	c 752	3	30.0	45	6	AR145061	AR145061 Sequence
c 680	3	30.0	33	6	AX190505	AX190505 Sequence	c 753	3	30.0	45	6	AR145065	AR145065 Sequence
681	3	30.0	33	6	BD010985	BD010985 HIV probe	c 754	3	30.0	45	6	AR145065	AR145065 Sequence
c 682	3	30.0	33	6	BD010985	BD010985 HIV probe	c 755	3	30.0	47	6	AR292054	AR292054 Sequence
683	3	30.0	33	6	BD010999	BD010999 HIV probe	c 756	3	30.0	47	6	AR292054	AR292054 Sequence
c 684	3	30.0	33	6	BD010999	BD010999 HIV probe	c 757	3	30.0	47	6	AR292054	AR292054 Sequence
685	3	30.0	33	6	BD011039	BD011039 HIV probe	c 758	3	30.0	48	6	AR028338	AR028338 Sequence
c 686	3	30.0	33	6	BD011039	BD011039 HIV probe	c 759	3	30.0	48	6	AR028338	AR028338 Sequence
687	3	30.0	34	6	AR150579	AR150579 Sequence	c 760	3	30.0	48	6	I24936	I24936 Sequence 8
c 688	3	30.0	34	6	AR150579	AR150579 Sequence	c 761	3	30.0	48	6	I24936	I24936 Sequence 8
689	3	30.0	34	6	AR350422	AR350422 Sequence	c 762	3	30.0	48	6	AR233640	AR233640 Sequence
c 690	3	30.0	34	6	AR350422	AR350422 Sequence	c 763	3	30.0	48	6	AR233640	AR233640 Sequence
691	3	30.0	34	6	AX955659	AX955659 Sequence	c 764	3	30.0	50	6	AR428987	AR428987 Sequence
c 692	3	30.0	34	6	AX955659	AX955659 Sequence	c 765	3	30.0	50	6	AR428987	AR428987 Sequence
693	3	30.0	35	6	AR156618	AR156618 Sequence	c 766	3	30.0	51	6	AR321782	AR321782 Sequence
c 694	3	30.0	35	6	AR156618	AR156618 Sequence	c 767	3	30.0	51	6	AR321782	AR321782 Sequence
695	3	30.0	35	6	ES1753	ES1753 Xylitol deh	c 768	3	30.0	51	6	AX911772	AX911772 Sequence
c 696	3	30.0	35	6	ES1753	ES1753 Xylitol deh	c 769	3	30.0	51	6	AX911772	AX911772 Sequence
697	3	30.0	35	6	AX739899	AX739899 Sequence	c 770	3	30.0	51	6	BD047305	BD047305 Sequence
c 698	3	30.0	35	6	AX739899	AX739899 Sequence	c 771	3	30.0	51	6	BD047305	BD047305 Sequence
699	3	30.0	35	6	AX781539	AX781539 Sequence	c 772	3	30.0	54	6	E37139	E37139 Method for
c 700	3	30.0	35	6	AX781539	AX781539 Sequence	c 773	3	30.0	54	6	E37139	E37139 Method for
701	3	30.0	35	6	AX817048	AX817048 Sequence	c 774	3	30.0	54	6	E37140	E37140 Method for
c 702	3	30.0	35	6	AX817048	AX817048 Sequence	c 775	3	30.0	54	6	E37140	E37140 Method for
703	3	30.0	36	6	AR013848	AR013848 Sequence	c 776	3	30.0	58	6	AR417144	AR417144 Sequence
c 704	3	30.0	36	6	AR013848	AR013848 Sequence	c 777	3	30.0	58	6	AR417144	AR417144 Sequence
705	3	30.0	36	6	AR033802	AR033802 Sequence	c 778	3	30.0	58	6	AX914166	AX914166 Sequence
c 706	3	30.0	36	6	AR033802	AR033802 Sequence	c 779	3	30.0	58	6	AX914166	AX914166 Sequence
707	3	30.0	36	6	AR042462	AR042462 Sequence	c 780	3	30.0	58	6	AX977838	AX977838 Sequence
c 708	3	30.0	36	6	AR042462	AR042462 Sequence	c 781	3	30.0	58	6	AX977838	AX977838 Sequence
709	3	30.0	36	6	AR058342	AR058342 Sequence	c 782	3	30.0	58	6	BD049699	BD049699 Sequence
c 710	3	30.0	36	6	AR058342	AR058342 Sequence	c 783	3	30.0	58	6	BD112697	BD112697 EST and e
711	3	30.0	36	6	AR060737	AR060737 Sequence	c 784	3	30.0	58	6	BD112697	BD112697 EST and e
c 712	3	30.0	36	6	AR060737	AR060737 Sequence	c 785	3	30.0	59	6	AR023546	AR023546 Sequence
713	3	30.0	36	6	AR068866	AR068866 Sequence	c 786	3	30.0	59	6	AR023546	AR023546 Sequence
c 714	3	30.0	36	6	AR068866	AR068866 Sequence	c 787	3	30.0	59	6	AR082654	AR082654 Sequence
715	3	30.0	36	6	AR088168	AR088168 Sequence	c 788	3	30.0	59	6	AR082654	AR082654 Sequence
c 716	3	30.0	36	6	AR088168	AR088168 Sequence	c 789	3	30.0	59	6	AR156181	AR156181 Sequence
717	3	30.0	37	6	AR024214	AR024214 Sequence	c 790	3	30.0	59	6	AR156181	AR156181 Sequence
c 718	3	30.0	37	6	AR024214	AR024214 Sequence	c 791	3	30.0	59	6	AR381063	AR381063 Sequence
719	3	30.0	38	6	CQ821249	CQ821249 Sequence	c 792	3	30.0	59	6	AR381063	AR381063 Sequence
c 720	3	30.0	38	6	CQ821249	CQ821249 Sequence	c 793	3	30.0	60	6	A62989	A62989 Sequence 1
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c 722	3	30.0	38	6	AR302751	AR302751 Sequence	c 795	3	30.0	61	6	AR165812	AR165812 Sequence
723	3	30.0	38	6	AX078765	AX078765 Sequence	c 796	3	30.0	61	6	AR165812	AR165812 Sequence
c 724	3	30.0	38	6	AX078765	AX078765 Sequence	c 797	3	30.0	61	6	AR305008	AR305008 Sequence
725	3	30.0	38	6	AX361208	AX361208 Sequence	c 798	3	30.0	61	6	AR305008	AR305008 Sequence
c 726	3	30.0	38	6	AX361208	AX361208 Sequence	c 799	3	30.0	61	6	AR423257	AR423257 Sequence
727	3	30.0	39	6	I44118	I44118 Sequence 5	c 800	3	30.0	61	6	AR423257	AR423257 Sequence
c 728	3	30.0	39	6	I44118	I44118 Sequence 5	c 801	3	30.0	61	6	AX983951	AX983951 Sequence
729	3	30.0	39	6	I48966	I48966 Sequence 5	c 802	3	30.0	61	6	AX983951	AX983951 Sequence
c 730	3	30.0	39	6	I48966	I48966 Sequence 5	c 803	3	30.0	61	6	BD118810	BD118810 EST and e
731	3	30.0	39	6	AR302246	AR302246 Sequence	c 804	3	30.0	61	6	BD118810	BD118810 EST and e
c 732	3	30.0	39	6	AR302246	AR302246 Sequence	c 805	3	30.0	63	6	AR393459	AR393459 Sequence
733	3	30.0	39	6	AR367375	AR367375 Sequence	c 806	3	30.0	63	6	AR393459	AR393459 Sequence
c 734	3	30.0	39	6	AR367375	AR367375 Sequence	c 807	3	30.0	64	6	AX909809	AX909809 Sequence
735	3	30.0	39	6	AR367379	AR367379 Sequence	c 808	3	30.0	64	6	AX909809	AX909809 Sequence
c 736	3	30.0	39	6	AR367379	AR367379 Sequence	c 809	3	30.0	64	6	BD045342	BD045342 Sequence
737	3	30.0	39	6	AX080329	AX080329 Sequence	c 810	3	30.0	64	6	BD045342	BD045342 Sequence
c 738	3	30.0	39	6	AX080329	AX080329 Sequence	c 811	3	30.0	66	6	A03733	A03733 Nucleotide
739	3	30.0	41	6	AX518947	AX518947 Sequence	c 812	3	30.0	66	6	A03733	A03733 Nucleotide
c 740	3	30.0	41	6	AX518947	AX518947 Sequence	c 813	3	30.0	68	6	AX900764	AX900764 Sequence
741	3	30.0	41	6	AX518948	AX518948 Sequence	c 814	3	30.0	68	6	AX900764	AX900764 Sequence
c 742	3	30.0	41	6	AX518948	AX518948 Sequence	c 815	3	30.0	68	6	BD036297	BD036297 Sequence
743	3	30.0	42	6	AR110339	AR110339 Sequence	c 816	3	30.0	68	6	BD036297	BD036297 Sequence
c 744	3	30.0	42	6	AR110339	AR110339 Sequence	c 817	3	30.0	69	6	AR149415	AR149415 Sequence
745	3	30.0	42	6	AR263795	AR263795 Sequence	c 818	3	30.0	69	6	AR149415	AR149415 Sequence
c 746	3	30.0	42	6	AR263795	AR263795 Sequence	c 819	3	30.0	69	6	AR149416	AR149416 Sequence
747	3	30.0	42	6	BD009359	BD009359 Chimeric,	c 820	3	30.0	69	6	AR149416	AR149416 Sequence
c 748	3	30.0	42	6	BD009359	BD009359 Chimeric,	c 821	3	30.0	70	6	AR165804	AR165804 Sequence
749	3	30.0	45	6	AR145060	AR145060 Sequence	c 822	3	30.0	70	6	AR165804	AR165804 Sequence



969 2 20.0 6 6 AX711257 Sequence  
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971 2 20.0 6 6 AX786596 Sequence  
c 972 2 20.0 6 6 AX786596 Sequence  
973 2 20.0 6 6 AX933919 Sequence  
c 974 2 20.0 6 6 AX933919 Sequence  
975 2 20.0 6 6 AX933921 Sequence  
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977 2 20.0 6 6 AX933934 Sequence  
c 978 2 20.0 6 6 AX933934 Sequence  
979 2 20.0 6 6 AX933945 Sequence  
c 980 2 20.0 6 6 AX933945 Sequence  
981 2 20.0 6 6 AX933946 Sequence  
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983 2 20.0 6 6 AX933951 Sequence  
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985 2 20.0 6 6 AX933954 Sequence  
c 986 2 20.0 6 6 AX933954 Sequence  
987 2 20.0 6 6 AX933955 Sequence  
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991 2 20.0 6 6 BD069912 Use of nu  
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997 2 20.0 7 6 BD261154 Methods a  
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999 2 20.0 7 6 BD261309 Methods a  
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## ALIGNMENTS

RESULT 1  
LOCUS A67159 10 bp DNA linear PAT 29-MAR-1999  
DEFINITION Sequence 16 from Patent WO9741433.  
ACCESSION A67159

VERSION A67159.1 GI:4538508

KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Kouzarides,T.  
TITLE METHOD AND MEANS FOR DISRUPTION OF p53 AND RB INTERACTION  
JOURNAL

FEATURES  
source  
1..10  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
Db 1 RRRCWGYYY 10  
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## RESULT 2

A67159/c  
LOCUS A67159 10 bp DNA linear PAT 29-MAR-1999  
DEFINITION Sequence 16 from Patent WO9741433.  
ACCESSION A67159

VERSION A67159.1 GI:4538508  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Kouzarides,T.  
TITLE METHOD AND MEANS FOR DISRUPTION OF p53 AND RB INTERACTION  
JOURNAL  
FEATURES  
source  
1..10  
Location/Qualifiers  
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## ORIGIN

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 RRRCWGYYY 1  
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## RESULT 3

AR003507  
LOCUS AR003507 10 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 3 from patent US 5744310.  
ACCESSION AR003507

VERSION AR003507.1 GI:3964766

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C.  
TITLE Bax promoter sequence and screening assays for indentifying agents  
that regulate bax gene expression

JOURNAL  
FEATURES  
source  
1..10  
Location/Qualifiers  
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## ORIGIN

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Db 1 RRRCWGYYY 10  
|||||

## RESULT 4

AR003507/c  
LOCUS AR003507 10 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 3 from patent US 5744310.  
ACCESSION AR003507

VERSION AR003507.1 GI:3964766

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C.  
TITLE Bax promoter sequence and screening assays for indentifying agents  
that regulate bax gene expression

JOURNAL  
FEATURES  
source  
1..10  
Location/Qualifiers

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ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 5
LOCUS      AR070749      10 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5908750.
ACCESSION  AR070749
VERSION     AR070749.1  GI:7221637
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Reed,J.C., Miyashita,T., Hariigai,M. and Hanada,M.
TITLE     Screening assays for identifying agents that regulate the
          expression of genes involved in cell death
JOURNAL    Patent: US 5908750-A 30 01-JUN-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 6
LOCUS      AR070749      10 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5908750.
ACCESSION  AR070749
VERSION     AR070749.1  GI:7221637
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Reed,J.C., Miyashita,T., Hariigai,M. and Hanada,M.
TITLE     Screening assays for identifying agents that regulate the
          expression of genes involved in cell death
JOURNAL    Patent: US 5908750-A 30 01-JUN-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 7
LOCUS      AR074547      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 3 from patent US 5955263.
ACCESSION  AR074547
VERSION     AR074547.1  GI:10001302
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
TITLE     Sequence specific DNA binding by p53
JOURNAL    Patent: US 5955263-A 3 21-SEP-1999;
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 8
LOCUS      AR074547      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 3 from patent US 5955263.
ACCESSION  AR074547
VERSION     AR074547.1  GI:10001302
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
TITLE     Sequence specific DNA binding by p53
JOURNAL    Patent: US 5955263-A 3 21-SEP-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 9
LOCUS      AR124219      10 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 29 from patent US 6171857.
ACCESSION  AR124219
VERSION     AR124219.1  GI:14109580
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Hendrickson,E.A.
TITLE     Leucine zipper protein, KARP-1 and methods of regulating DNA
          dependent protein kinase activity
JOURNAL    Patent: US 6171857-A 29 09-JAN-2001;
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGGYY 10  
|||||  
Db 1 RRCWGGYY 10  
|||||

RESULT 10  
AR124219/c 10 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 29 from patent US 6171857.  
ACCESSION AR124219  
VERSION AR124219.1 GI:14109580  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hendrickson,E.A.  
TITLE Leucine zipper protein, KARP-1 and methods of regulating DNA  
dependent protein kinase activity  
JOURNAL Patent: US 6171857-A 29 09-JAN-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 10 RRCWGGYY 1  
|||||

RESULT 11  
AR157427 10 bp DNA linear PAT 17-OCT-2001  
LOCUS  
DEFINITION Sequence 3 from patent US 6245515.  
ACCESSION AR157427  
VERSION AR157427.1 GI:16218366  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Vogelstein,B., Kinzler,K.W. and Sherman,M.I.  
TITLE Sequence specific DNA binding p53  
JOURNAL Patent: US 6245515-A 3 12-JUN-2001;  
FEATURES Location/Qualifiers  
source 1. .10  
/organism="unknown"  
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Query Match 100.0%; Score 10; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGGYY 10  
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Db 1 RRCWGGYY 10  
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RESULT 12  
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LOCUS  
DEFINITION Sequence 3 from patent US 6245515.  
ACCESSION AR157427  
VERSION AR157427.1 GI:16218366  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Vogelstein,B., Kinzler,K.W. and Sherman,M.I.  
TITLE Sequence specific DNA binding p53  
JOURNAL Patent: US 6245515-A 3 12-JUN-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 RRCWGGYY 1  
|||||

RESULT 13  
I62424 10 bp DNA linear PAT 07-OCT-1997  
LOCUS  
DEFINITION Sequence 30 from patent US 5659024.  
ACCESSION I62424  
VERSION I62424.1 GI:2480372  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.  
TITLE Promoters that regulate the expression of genes involved in cell  
death  
JOURNAL Patent: US 5659024-A 30 19-AUG-1997;  
FEATURES Location/Qualifiers  
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Db 1 RRCWGGYY 10  
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RESULT 14  
I62424/c 10 bp DNA linear PAT 07-OCT-1997  
LOCUS  
DEFINITION Sequence 30 from patent US 5659024.  
ACCESSION I62424  
VERSION I62424.1 GI:2480372  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.  
TITLE Promoters that regulate the expression of genes involved in cell

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death
JOURNAL Patent: US 5659024-A 30 19-AUG-1997;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
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Db 10 RRCWGWYYY 1

RESULT 15
AR303877
LOCUS AR303877 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 24 from patent US 6544746.
ACCESSION AR303877
VERSION AR303877.1 GI:31692655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Heyduk,T.
TITLE Rapid and sensitive proximity-based assay for the detection and
quantification of DNA binding proteins
JOURNAL Patent: US 6544746-A 24 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
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/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
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Db 1 RRCWGWYYY 10

RESULT 16
AR303877/c
LOCUS AR303877 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 24 from patent US 6544746.
ACCESSION AR303877
VERSION AR303877.1 GI:31692655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Heyduk,T.
TITLE Rapid and sensitive proximity-based assay for the detection and
quantification of DNA binding proteins
JOURNAL Patent: US 6544746-A 24 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
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/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
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Db 1 RRCWGWYYY 10

RESULT 17
AR303877
LOCUS AR303877 10 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0105421.
ACCESSION AR303877
VERSION AR303877.1 GI:13121849
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS de la cueva Mendez,G.C., Laskey,R.A., Mills,A.D. and diaz
Orejas,R.C.
TITLE Methods employing bacterial toxin-antitoxin systems for killing
eukaryotic cells
JOURNAL Patent: WO 0105421-A 1 25-JAN-2001;
FEATURES Location/Qualifiers
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Db 1 RRCWGWYYY 10

RESULT 18
AR303877/c
LOCUS AR303877 10 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0105421.
ACCESSION AR303877
VERSION AR303877.1 GI:13121849
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS de la cueva Mendez,G.C., Laskey,R.A., Mills,A.D. and diaz
Orejas,R.C.
TITLE Methods employing bacterial toxin-antitoxin systems for killing
eukaryotic cells
JOURNAL Patent: WO 0105421-A 1 25-JAN-2001;
FEATURES Location/Qualifiers
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/note="Consensus sequence"

ORIGIN
Query Match 100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
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Db 10 RRCWGWYYY 10

RESULT 19
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AX339211  
LOCUS AX339211 10 bp DNA linear PAT 10-JAN-2002  
DEFINITION Sequence 5 from Patent WO0196602.  
ACCESSION AX339211  
VERSION AX339211.1 GI:18135472  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Yang, A.L. and Festing, M.  
TITLE Methods and materials to determine the p53 status of a sample by determining the binding of p53 to a vector  
JOURNAL Patent: WO 0196602-A 5 20-DEC-2001;  
MEDICAL RESEARCH COUNCIL (GB)  
FEATURES  
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Db 1 RRCWGWYYY 10  
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DEFINITION Sequence 5 from Patent WO0196602.  
ACCESSION AX339211  
VERSION AX339211.1 GI:18135472  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Yang, A.L. and Festing, M.  
TITLE Methods and materials to determine the p53 status of a sample by determining the binding of p53 to a vector  
JOURNAL Patent: WO 0196602-A 5 20-DEC-2001;  
MEDICAL RESEARCH COUNCIL (GB)  
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/db\_xref="taxon:32630"  
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QY 1 RRCWGWYYY 10  
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Db 1 RRCWGWYYY 10  
RESULT 21  
AX776278  
LOCUS AX776278 10 bp DNA linear PAT 14-JUL-2003  
DEFINITION Sequence 14 from Patent WO03048361.  
ACCESSION AX776278  
VERSION AX776278.1 GI:32693933  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Hayes, I., Cotter, T., Murphy, F. and Seery, L.  
TITLE Early stage radox-related apoptosis modulator-2 (esram-2)  
JOURNAL Patent: WO 03054010-A 14 03-JUL-2003;  
Eirx Therapeutics Ltd (IE)  
FEATURES  
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/note="Mammalian p53 recognition site"

ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Hayes, I., Cotter, T., Murphy, F. and Seery, L.  
TITLE P55pik  
JOURNAL Patent: WO 03048361-A 14 12-JUN-2003;  
Eirx Therapeutics Ltd (IE)  
FEATURES  
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 RRCWGWYYY 10  
RESULT 22  
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LOCUS AX776278 10 bp DNA linear PAT 14-JUL-2003  
DEFINITION Sequence 14 from Patent WO03048361.  
ACCESSION AX776278  
VERSION AX776278.1 GI:32693933  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Hayes, I., Cotter, T., Murphy, F. and Seery, L.  
TITLE P55pik  
JOURNAL Patent: WO 03048361-A 14 12-JUN-2003;  
Eirx Therapeutics Ltd (IE)  
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Db 10 RRCWGWYYY 1  
RESULT 23  
AX803572  
LOCUS AX803572 10 bp DNA linear PAT 24-NOV-2003  
DEFINITION Sequence 14 from Patent WO03054010.  
ACCESSION AX803572  
VERSION AX803572.1 GI:38502146  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Hayes, I., Cotter, T., Murphy, F. and Seery, L.  
TITLE Early stage radox-related apoptosis modulator-2 (esram-2)  
JOURNAL Patent: WO 03054010-A 14 03-JUL-2003;  
Eirx Therapeutics Ltd (IE)  
FEATURES  
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/db\_xref="taxon:32630"  
/note="Mammalian p53 recognition site"



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/organism="unidentified"
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ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRRCWGGYYY 10
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Db      1 RRRRCWGGYYY 10

RESULT 24
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LOCUS      AX803572      10 bp      DNA      linear      PAT 24-NOV-2003
DEFINITION Sequence 14 from Patent WO03054010.
ACCESSION  AX803572
VERSION     AX803572.1 GI:38502146
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1
AUTHORS     Hayes,I., Cotter,T., Murphy,F. and Seely,L.
TITLE       Early stage redox-related apoptosis modulator-2 (esram-2)
JOURNAL     Patent: WO 03054010-A 14 03-JUL-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES   source
            location/Qualifiers
            1..10
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="mammalian-Mammalian p53 recognition site"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRRCWGGYYY 10
      |||||
Db      10 RRRRCWGGYYY 1

RESULT 25
BD064950
LOCUS      BD064950      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION  BD064950
VERSION     BD064950.1 GI:22610553
KEYWORDS   JP 2001275678-A/162.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
            1 (bases 1 to 10)
REFERENCE   1
AUTHORS     Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
TITLE       Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
JOURNAL     Patent: JP 2001275678-A 162 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS Artificial Sequence
            PN JP 2001275678-A/162
            PD 09-OCT-2001
            PF 31-MAR-2000 JP 2000096306
            PI TOSHIIKO KISHIMOTO, SHINICHIRO NIWA, YUKO MORI, SACHIYO PI
            MI KAZUKO NISHIKAWA
            PC C12N15/09, C12N5/10, C12Q1/00, C12Q1/68, C12N15/00, C12N5/00 CC

Synthetic DNA
FH Key      Location/Qualifiers
FT source    1..10
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

FEATURES   source
            Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRRCWGGYYY 10
      |||||
Db      10 RRRRCWGGYYY 1

RESULT 27
BD084759
LOCUS      BD084759      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION  BD084759
VERSION     BD084759.1 GI:22630369
KEYWORDS   JP 2001521375-A/57.

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Synthetic DNA
FH Key      Location/Qualifiers
FT source    1..10
            /organism="Artificial Sequence".

FEATURES   source
            Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRRCWGGYYY 10
      |||||
Db      1 RRRRCWGGYYY 10

RESULT 26
BD064950/c
LOCUS      BD064950      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION  BD064950
VERSION     BD064950.1 GI:22610553
KEYWORDS   JP 2001275678-A/162.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
            1 (bases 1 to 10)
REFERENCE   1
AUTHORS     Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
TITLE       Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
JOURNAL     Patent: JP 2001275678-A 162 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS Artificial Sequence
            PN JP 2001275678-A/162
            PD 09-OCT-2001
            PF 31-MAR-2000 JP 2000096306
            PI TOSHIIKO KISHIMOTO, SHINICHIRO NIWA, YUKO MORI, SACHIYO PI
            MI KAZUKO NISHIKAWA
            PC C12N15/09, C12N5/10, C12Q1/00, C12Q1/68, C12N15/00, C12N5/00 CC

Synthetic DNA
FH Key      Location/Qualifiers
FT source    1..10
            /organism="Artificial Sequence".

FEATURES   source
            Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRRCWGGYYY 10
      |||||
Db      10 RRRRCWGGYYY 1

RESULT 27
BD084759
LOCUS      BD084759      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION  BD084759
VERSION     BD084759.1 GI:22630369
KEYWORDS   JP 2001521375-A/57.

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SOURCE      unidentified
ORGANISM      unidentified
unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
TITLE      Human nerve growth factor exon 1 and exon 3 promoters
JOURNAL      Patent: JP 2001521375-A 57 06-NOV-2001;
              HOECHST MARION ROUSSEL INC
COMMENT      OS Unidentified
              PN JP 2001521375-A/57
              PD 06-NOV-2001
              PF 12-JAN-1998 JP 1998534446
              PR 06-FEB-1997 US 60/038212
              PI MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN PI
              SUBRAMANIAM
              PC C07K14/48,C12Q1/68
              CC Strandedness: Double;
              CC Topology: Unknown;
              CC Human nerve growth factor exon 1 and exon 3 promoters FH Key
              FT source 1..10
              FT Location/Qualifiers
                 Location/Qualifiers
                 1..10
                 /organism='Unidentified'.
                 /organism="unidentified"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10
Db 1 RRCRCWGGYY 10

RESULT 28
BD084759/c
LOCUS      Human nerve growth factor exon 1 and exon 3 promoters.
DEFINITION BD084759
ACCESSION  BD084759.1 GI:22630369
VERSION     JP 2001521375-A/57.
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
TITLE      Human nerve growth factor exon 1 and exon 3 promoters
JOURNAL      Patent: JP 2001521375-A 57 06-NOV-2001;
              HOECHST MARION ROUSSEL INC
COMMENT      OS Unidentified
              PN JP 2001521375-A/57
              PD 06-NOV-2001
              PF 12-JAN-1998 JP 1998534446
              PR 06-FEB-1997 US 60/038212
              PI MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN PI
              SUBRAMANIAM
              PC C07K14/48,C12Q1/68
              CC Strandedness: Double;
              CC Topology: Unknown;
              CC Human nerve growth factor exon 1 and exon 3 promoters FH Key
              FT source 1..10
              FT Location/Qualifiers
                 Location/Qualifiers
                 1..10
                 /organism='Unidentified'.
                 /organism="unidentified"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10
Db 1 RRCRCWGGYY 10

RESULT 29
BD084759/c
LOCUS      Human nerve growth factor exon 1 and exon 3 promoters.
DEFINITION BD084759
ACCESSION  BD084759.1 GI:22630369
VERSION     JP 2001521375-A/57.
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
TITLE      Human nerve growth factor exon 1 and exon 3 promoters
JOURNAL      Patent: JP 2001521375-A 57 06-NOV-2001;
              HOECHST MARION ROUSSEL INC
COMMENT      OS Unidentified
              PN JP 2001521375-A/57
              PD 06-NOV-2001
              PF 12-JAN-1998 JP 1998534446
              PR 06-FEB-1997 US 60/038212
              PI MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN PI
              SUBRAMANIAM
              PC C07K14/48,C12Q1/68
              CC Strandedness: Double;
              CC Topology: Unknown;
              CC Human nerve growth factor exon 1 and exon 3 promoters FH Key
              FT source 1..10
              FT Location/Qualifiers
                 Location/Qualifiers
                 1..10
                 /organism='Unidentified'.
                 /organism="unidentified"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10
Db 1 RRCRCWGGYY 10

RESULT 29
AX685336
LOCUS      Sequence 26 from Patent WO02064790.
DEFINITION AX685336
ACCESSION  AX685336
VERSION     AX685336.1 GI:29371660
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Yu,J., Kinzler,K.W. and Vogelstein,B.
TITLE      Jf1 protein induces rapid apoptosis
JOURNAL      Patent: WO 02064790-A 26 22-AUG-2002;
              The Johns Hopkins University (US)
FEATURES      Location/Qualifiers
                 source
                 1..19
                 /organism="Homo sapiens"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10
Db 10 RRCRCWGGYY 19

RESULT 30
AX685336/c
LOCUS      Sequence 26 from Patent WO02064790.
DEFINITION AX685336
ACCESSION  AX685336
VERSION     AX685336.1 GI:29371660
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Yu,J., Kinzler,K.W. and Vogelstein,B.
TITLE      Jf1 protein induces rapid apoptosis
JOURNAL      Patent: WO 02064790-A 26 22-AUG-2002;
              The Johns Hopkins University (US)
FEATURES      Location/Qualifiers
                 source
                 1..19
                 /organism="Homo sapiens"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10
Db 19 RRCRCWGGYY 10
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RESULT 31
AR181179
LOCUS       AR181179                20 bp    DNA          linear    PAT 20-APR-2002
DEFINITION   Sequence 6 from patent US 6335156.
ACCESSION   AR181179
VERSION     AR181179.1  GI:20223393
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Heremking,H., Vogelstein,B. and Kinzler,K.W.
TITLE       14-3-3.sigma. arrests the cell cycle
JOURNAL     Patent: US 6335156-A 6 01-JAN-2002;
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYYY 10
       |||||
Db      1 RRRCWGYYY 10

RESULT 32
AR181179/c
LOCUS       AR181179                20 bp    DNA          linear    PAT 20-APR-2002
DEFINITION   Sequence 6 from patent US 6335156.
ACCESSION   AR181179
VERSION     AR181179.1  GI:20223393
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Heremking,H., Vogelstein,B. and Kinzler,K.W.
TITLE       14-3-3.sigma. arrests the cell cycle
JOURNAL     Patent: US 6335156-A 6 01-JAN-2002;
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYYY 10
       |||||
Db      1 RRRCWGYYY 10

RESULT 33
AR060431
LOCUS       AR060431                21 bp    DNA          linear    PAT 29-SEP-1999
DEFINITION   Sequence 4 from patent US 5840673.
ACCESSION   AR060431
VERSION     AR060431.1  GI:5986881
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 21)
AUTHORS     Buckbinder,L.R., Kley,N. and Seizinger,B.R.
TITLE       Insulin-like growth factor binding protein 3 (IGF-BP3) in treatment
JOURNAL     Patent: US 5840673-A 4 24-NOV-1998;
FEATURES    Location/Qualifiers
             source
               1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYYY 10
       |||||
Db      21 RRRCWGYYY 12

RESULT 34
AR060431/c
LOCUS       AR060431                21 bp    DNA          linear    PAT 29-SEP-1999
DEFINITION   Sequence 4 from patent US 5840673.
ACCESSION   AR060431
VERSION     AR060431.1  GI:5986881
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 21)
AUTHORS     Buckbinder,L.R., Kley,N. and Seizinger,B.R.
TITLE       Insulin-like growth factor binding protein 3 (IGF-BP3) in treatment
JOURNAL     Patent: US 5840673-A 4 24-NOV-1998;
FEATURES    Location/Qualifiers
             source
               1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 10; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYYY 10
       |||||
Db      21 RRRCWGYYY 12

RESULT 35
I22646
LOCUS       I22646                  20 bp    DNA          linear    PAT 07-OCT-1996
DEFINITION   Sequence 134 from patent US 5527898.
ACCESSION   I22646
VERSION     I22646.1  GI:1603000
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
             Resnick,R.M. and Zhang,T.Y.
TITLE       Detection of human papillomavirus by the polymerase chain reaction
JOURNAL     Patent: US 5527898-A 134 18-JUN-1996;
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      50.0%; Score 5; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 WGGYY 9
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Db          11  WWCYY 15

RESULT 36
LOCUS      122646/c
DEFINITION Sequence 134 from patent US 5527899.
ACCESSION  122646
VERSION    122646.1 GI:1603000
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
           Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5527898-A 134 18-JUN-1996;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      50.0%; Score 5; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRCWW 6
      |||||
Db      15 RRCWW 11

RESULT 37
LOCUS      147471
DEFINITION Sequence 134 from patent US 5639871.
ACCESSION  147471
VERSION    147471.1 GI:2471436
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
           Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 134 17-JUN-1997;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      50.0%; Score 5; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRCWW 6
      |||||
Db      15 RRCWW 11

RESULT 38
LOCUS      147471/c
DEFINITION Sequence 134 from patent US 5639871.
ACCESSION  147471
VERSION    147471.1 GI:2471436
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
           Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 134 17-JUN-1997;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      50.0%; Score 5; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWCYY 9
      |||||
Db      11 WWCYY 15

RESULT 39
LOCUS      CQ771564
DEFINITION Sequence 1 from Patent EP1138781.
ACCESSION  CQ771564
VERSION    CQ771564.1 GI:45125554
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   Kulesz-Martin,M.F. and Liu,Y.
REFERENCE  1
AUTHORS   Kulesz-Martin,M.F. and Liu,Y.
TITLE     Method for Quantifying DNA binding activity of DNA binding proteins
JOURNAL   Patent: EP 1138781-A 1 04-OCT-2001;
           HEALTH RESEARCH, INC. (US)
FEATURES   Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Specific to p53 protein; p53 consensus sequence"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRC 4
      |||||
Db      1 RRRC 4

RESULT 40
LOCUS      CQ771564/c
DEFINITION Sequence 1 from Patent EP1138781.
ACCESSION  CQ771564
VERSION    CQ771564.1 GI:45125554
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   Kulesz-Martin,M.F. and Liu,Y.
REFERENCE  1
AUTHORS   Kulesz-Martin,M.F. and Liu,Y.
TITLE     Method for Quantifying DNA binding activity of DNA binding proteins
JOURNAL   Patent: EP 1138781-A 1 04-OCT-2001;
           HEALTH RESEARCH, INC. (US)
FEATURES   Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Specific to p53 protein; p53 consensus sequence"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRC 4
      |||||
Db      1 RRRC 4

RESULT 41
LOCUS      CQ771564
DEFINITION Sequence 1 from Patent EP1138781.
ACCESSION  CQ771564
VERSION    CQ771564.1 GI:45125554
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   Kulesz-Martin,M.F. and Liu,Y.
REFERENCE  1
AUTHORS   Kulesz-Martin,M.F. and Liu,Y.
TITLE     Method for Quantifying DNA binding activity of DNA binding proteins
JOURNAL   Patent: EP 1138781-A 1 04-OCT-2001;
           HEALTH RESEARCH, INC. (US)
FEATURES   Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Specific to p53 protein; p53 consensus sequence"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRC 4
      |||||
Db      1 RRRC 4

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ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4
    ||||
Db 10 RRRR 7

RESULT 41
I74680
LOCUS          I74680          10 bp      DNA          linear          PAT 03-APR-1998
DEFINITION     Sequence 9 from patent US 5688918.
ACCESSION      I74680
VERSION        I74680.1 GI:3010821
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Kulesz-Martin,M.F.
TITLE          p53as protein and antibody therefor
JOURNAL        Patent: US 5688918-A 9 18-NOV-1997;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWGG 7
    ||||
Db 4 CWGG 7

RESULT 42
I74680/c
LOCUS          I74680          10 bp      DNA          linear          PAT 03-APR-1998
DEFINITION     Sequence 9 from patent US 5688918.
ACCESSION      I74680
VERSION        I74680.1 GI:3010821
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Kulesz-Martin,M.F.
TITLE          p53as protein and antibody therefor
JOURNAL        Patent: US 5688918-A 9 18-NOV-1997;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWGG 7
    ||||
Db 4 CWGG 7

RESULT 43
I74680
LOCUS          I74680          10 bp      DNA          linear          PAT 01-DEC-1998
DEFINITION     Sequence 9 from patent US 5726024.

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ACCESSION      I91766
VERSION        I91766.1 GI:3936236
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Kulesz-Martin,M.F.
TITLE          p53as protein and antibody therefor
JOURNAL        Patent: US 5726024-A 9 10-MAR-1998;
FEATURES       Location/Qualifiers
                source
                1..10
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                /mol_type="unassigned DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWGG 7
    ||||
Db 4 CWGG 7

RESULT 44
I91766/c
LOCUS          I91766          10 bp      DNA          linear          PAT 01-DEC-1998
DEFINITION     Sequence 9 from patent US 5726024.
ACCESSION      I91766
VERSION        I91766.1 GI:3936236
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Kulesz-Martin,M.F.
TITLE          p53as protein and antibody therefor
JOURNAL        Patent: US 5726024-A 9 10-MAR-1998;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWGG 7
    ||||
Db 7 CWGG 4

RESULT 45
BD090936
LOCUS          BD090936          10 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     Method for quantifying DNA binding activity of DNA binding
                proteins.
ACCESSION      BD090936
VERSION        BD090936.1 GI:22636546
KEYWORDS       JP 2001321199-A/1.
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Martin,M.F.K. and Liu,Y.
TITLE          Method for quantifying DNA binding activity of DNA binding proteins
JOURNAL        Patent: JP 2001321199-A 1 20-NOV-2001;
                HEALTH RESEARCH INC
COMMENT         OS Artificial Sequence
                PN JP 2001321199-A/1
                PD 20-NOV-2001

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PF 02-APR-2001 JP 2001103067
PR 31-MAR-2000 US 09/539945
PI MOLLY F KULESZ MARTIN,YUANGANG LIU
PC C12Q1/68,C07K14/47,C12N15/09,G01N33/15,G01N33/53, PC
G01N33/566//
PC C12M1/00,C12M1/20,C12M1/34,C12N15/00
CC Method for quantifying DNA binding activity of DNA binding CC
proteins
FH Key Location/Qualifiers
FT source 1..10
TITLE Location/Qualifiers
SOURCE /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4
|||
Db 1 RRC 4

RESULT 46
BD090936/c
LOCUS
DEFINITION
Method for quantifying DNA binding activity of DNA binding
proteins.
ACCESSION
BD090936.1 GI:22636546
VERSION
JP 2001321199-A/1.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Martin,M.F.K. and Liu,Y.
TITLE
Method for quantifying DNA binding activity of DNA binding proteins
JOURNAL
Patent: JP 2001321199-A 1 20-NOV-2001;
HEALTH RESEARCH INC
COMMENT
OS Artificial Sequence
PN JP 2001321199-A/1
PD 20-NOV-2001
PF 02-APR-2001 JP 2001103067
PR 31-MAR-2000 US 09/539945
PI MOLLY F KULESZ MARTIN,YUANGANG LIU
PC C12Q1/68,C07K14/47,C12N15/09,G01N33/15,G01N33/53, PC
G01N33/566//
PC C12M1/00,C12M1/20,C12M1/34,C12N15/00
CC Method for quantifying DNA binding activity of DNA binding CC
proteins
FH Key Location/Qualifiers
FT source 1..10
TITLE Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4
|||
Db 10 RRC 7

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RESULT 47
BD084901
LOCUS
DEFINITION
Characterising DNA.
ACCESSION
BD084901
VERSION
BD084901.1 GI:22630511
KEYWORDS
JP 2001521398-A/7.
SOURCE
synthetic construct
artificial sequences.
ORGANISM
1 (bases 1 to 12)
REFERENCE
Schmidt,G. and Thompson,A.H.
AUTHORS
Characterising DNA
TITLE
Patent: JP 2001521398-A 7 06-NOV-2001;
JOURNAL
BRAX GROUP LTD
COMMENT
OS Artificial Sequence
PN JP 2001521398-A/7
PD 06-NOV-2001
PF 20-APR-1998 JP 1998545274
PR 21-APR-1997 GB 9707980.0
PI GUNTER SCHMIDT,ANDREW HUGIN THOMPSON
PC C12Q1/68
CC Adapter oligonucleotide comprising a recognition site for a
sampling
CC cleavage agent
CC Key Location/Qualifiers
FH Key (1)..(12).
FT unsure Location/Qualifiers
SOURCE 1..12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 10
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Db 8 GYY 11

RESULT 48
BD084901/c
LOCUS
DEFINITION
Characterising DNA.
ACCESSION
BD084901
VERSION
BD084901.1 GI:22630511
KEYWORDS
JP 2001521398-A/7.
SOURCE
synthetic construct
artificial sequences.
ORGANISM
1 (bases 1 to 12)
REFERENCE
Schmidt,G. and Thompson,A.H.
AUTHORS
Characterising DNA
TITLE
Patent: JP 2001521398-A 7 06-NOV-2001;
JOURNAL
BRAX GROUP LTD
COMMENT
OS Artificial Sequence
PN JP 2001521398-A/7
PD 06-NOV-2001
PF 20-APR-1998 JP 1998545274
PR 21-APR-1997 GB 9707980.0
PI GUNTER SCHMIDT,ANDREW HUGIN THOMPSON
PC C12Q1/68
CC Adapter oligonucleotide comprising a recognition site for a
sampling
CC cleavage agent
CC Key Location/Qualifiers
FH Key (1)..(12).
FT unsure Location/Qualifiers
SOURCE 1..12
/organism="synthetic construct"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRR 4
    ||||
Db 11 RRRR 8

RESULT 49
AR451567
LOCUS AR451567 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 212 from patent US 6673917.
ACCESSION AR451567
VERSION AR451567.1 GI:42682592
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense IAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 212 06-JAN-2004;
FEATURES
    Location/Qualifiers
        source
            1..19
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
    ||||
Db 16 GYYY 19

RESULT 50
AR451567/c
LOCUS AR451567/c 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 212 from patent US 6673917.
ACCESSION AR451567
VERSION AR451567.1 GI:42682592
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense IAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 212 06-JAN-2004;
FEATURES
    Location/Qualifiers
        source
            1..19
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRR 4
    ||||
Db 19 RRRR 16

RESULT 51
AX412112
LOCUS AX412112 20 bp DNA linear PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papilloma
viruses.
ACCESSION BD184677
VERSION BD184677.1 GI:31876877
KEYWORDS JP 2002360271-A/656.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,

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LOCUS AX412112 19 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 212 from Patent WO0226968.
ACCESSION AX412112
VERSION AX412112.1 GI:21444577
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 212 04-APR-2002;
        University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES
    Location/Qualifiers
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            1..19
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
    ||||
Db 16 GYYY 19

RESULT 52
AX412112/c
LOCUS AX412112/c 19 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 212 from Patent WO0226968.
ACCESSION AX412112
VERSION AX412112.1 GI:21444577
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 212 04-APR-2002;
        University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES
    Location/Qualifiers
        source
            1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRR 4
    ||||
Db 19 RRRR 16

RESULT 53
BD184677
LOCUS BD184677 20 bp DNA linear PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papilloma
viruses.
ACCESSION BD184677
VERSION BD184677.1 GI:31876877
KEYWORDS JP 2002360271-A/656.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,

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TITLE Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.  
 JOURNAL Method and detector for identifying subtypes of human papilloma  
 Patent: JP 2002360271-A 656 17-DEC-2002;  
 COMMENT KING CAR FOOD INDUSTRIAL CO LTD  
 OS Artificial Sequence  
 PN JP 2002360271-A/656  
 PD 17-DEC-2002  
 PF 28-NOV-2001 JP 2001362595  
 PR 04-MAY-2001 TW 90110785  
 PI CHING-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSUAN HUANG, BOW-  
 HAENG LEE.  
 PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-  
 WEN SHI,  
 PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN  
 PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC  
 , C12Q1/70, G01N21/64,  
 PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1:93),  
 CC C12Q1/70, C12R1:93), C12N15/00, C12N15/00  
 CC E1 350L primer.  
 FH Key Location/Qualifiers  
 FT source 1. .20  
 /organism="Artificial Sequence".  
 FT Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 40.0%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GYYY 10  
 ||||  
 Db 6 GYYY 9

RESULT 54  
 BD184677/c  
 LOCUS 20 bp DNA linear PAT 17-JUN-2003  
 DEFINITION Method and detector for identifying subtypes of human papilloma  
 viruses  
 BD184677  
 BD184677.1 GI:31876977  
 VERSION JP 2002360271-A/656.  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,  
 Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.  
 TITLE Method and detector for identifying subtypes of human papilloma  
 JOURNAL Patent: JP 2002360271-A 656 17-DEC-2002;  
 COMMENT KING CAR FOOD INDUSTRIAL CO LTD  
 OS Artificial Sequence  
 PN JP 2002360271-A/656  
 PD 17-DEC-2002  
 PF 28-NOV-2001 JP 2001362595  
 PR 04-MAY-2001 TW 90110785  
 PI CHING-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSUAN HUANG, BOW-  
 HAENG LEE.  
 PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-  
 WEN SHI,  
 PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN  
 PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC  
 , C12Q1/70, G01N21/64,  
 PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1:93),  
 CC C12Q1/70, C12R1:93), C12N15/00, C12N15/00  
 CC E1 350L primer.  
 FH Key Location/Qualifiers  
 FT source 1. .20  
 /organism="Artificial Sequence".

FEATURES  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 40.0%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRRR 4  
 ||||  
 Db 9 RRRR 6

RESULT 55  
 I22645  
 LOCUS Sequence 133 from patent US 5527898.  
 DEFINITION I22645  
 ACCESSION I22645  
 VERSION I22645.1 GI:1602999  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,  
 Resnick,R.M. and Zhang,T.Y.  
 TITLE Detection of human papillomavirus by the polymerase chain reaction  
 JOURNAL Patent: US 5527898-A 133 18-JUN-1996;  
 FEATURES Location/Qualifiers  
 1. .20  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 40.0%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 WWGY 8  
 ||||  
 Db 11 WWGY 14

RESULT 56  
 I22645/c  
 LOCUS Sequence 133 from patent US 5527898.  
 DEFINITION I22645  
 ACCESSION I22645  
 VERSION I22645.1 GI:1602999  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,  
 Resnick,R.M. and Zhang,T.Y.  
 TITLE Detection of human papillomavirus by the polymerase chain reaction  
 JOURNAL Patent: US 5527898-A 133 18-JUN-1996;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"

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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 RCWW 6  
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Db          14 RCWW 11

RESULT 57
122647
LOCUS       122647          20 bp      DNA
DEFINITION  Sequence 135 from patent US 5527898.
ACCESSION  122647
VERSION    122647.1  GI:1603001
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5527898-A 135 18-JUN-1996;
FEATURES   Location/Qualifiers
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              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 9
        ||||
Db      12 WGY 15

RESULT 58
122647/c
LOCUS       122647          20 bp      DNA
DEFINITION  Sequence 135 from patent US 5527898.
ACCESSION  122647
VERSION    122647.1  GI:1603001
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5527898-A 135 18-JUN-1996;
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 9
        ||||
Db      12 WGY 15

RESULT 59
147470
LOCUS       147470          20 bp      DNA
DEFINITION  Sequence 133 from patent US 5639871.
ACCESSION  147470
VERSION    147470.1  GI:2471435
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RCW 5
        ||||
Db      15 RCW 12

RESULT 60
147470/c
LOCUS       147470          20 bp      DNA
DEFINITION  Sequence 133 from patent US 5639871.
ACCESSION  147470
VERSION    147470.1  GI:2471435
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 6
        ||||
Db      14 RCW 11

RESULT 61
147472
LOCUS       147472          20 bp      DNA
DEFINITION  Sequence 135 from patent US 5639871.
ACCESSION  147472
VERSION    147472.1  GI:2471437
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 135 17-JUN-1997;
FEATURES   Location/Qualifiers
            source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 6
        ||||
Db      14 RCW 11

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REFERENCE 1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES   Location/Qualifiers
            source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WGY 8
        ||||
Db      11 WGY 14

RESULT 60
147470/c
LOCUS       147470          20 bp      DNA
DEFINITION  Sequence 133 from patent US 5639871.
ACCESSION  147470
VERSION    147470.1  GI:2471435
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES   Location/Qualifiers
            source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 6
        ||||
Db      14 RCW 11

RESULT 61
147472
LOCUS       147472          20 bp      DNA
DEFINITION  Sequence 135 from patent US 5639871.
ACCESSION  147472
VERSION    147472.1  GI:2471437
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE     Detection of human papillomavirus by the polymerase chain reaction
JOURNAL   Patent: US 5639871-A 135 17-JUN-1997;
FEATURES   Location/Qualifiers
            source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 6
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Db      14 RCW 11

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGY 9  
Db 12 WGY 15

RESULT 62  
I47472/c

LOCUS I47472 20 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 135 from patent US 5639871.

ACCESSION I47472

VERSION I47472.1 GI:2471437

KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bauer, H.M., Gravitt, P.E., Greer, C.E., Impraia, C.C.,  
Manos, M.Michele., Resnick, R.M. and Zhang, T.Yi.

TITLE Detection of human papillomavirus by the polymerase chain reaction

JOURNAL Patent: US 5639871-A 135 17-JUN-1997;

FEATURES  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 40.0%; Score 4; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 REC 5  
Db 15 REC 12

RESULT 63  
AR030183

LOCUS AR030183 27 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 7 from patent US 5861245.

ACCESSION AR030183

VERSION AR030183.1 GI:5943397

KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)

AUTHORS McClelland, M., Welsh, J. Thomas. and Sorge, J.A.

TITLE Arbitrarily primed polymerase chain reaction method for fingerprinting genomes

JOURNAL Patent: US 5861245-A 7 19-JAN-1999;

FEATURES  
Location/Qualifiers  
1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 40.0%; Score 4; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4  
Db 15 RRRC 18

RESULT 64  
AR030183/c

LOCUS AR030183 27 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 7 from patent US 5861245.

ACCESSION AR030183

VERSION AR030183.1 GI:5943397

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)

AUTHORS McClelland, M., Welsh, J. Thomas. and Sorge, J.A.

TITLE Arbitrarily primed polymerase chain reaction method for fingerprinting genomes

JOURNAL Patent: US 5861245-A 7 19-JAN-1999;

FEATURES  
Location/Qualifiers  
1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 40.0%; Score 4; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 10  
Db 18 GYY 15

RESULT 65  
AR030187

LOCUS AR030187 27 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 11 from patent US 5861245.

ACCESSION AR030187

VERSION AR030187.1 GI:5943401

KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)

AUTHORS McClelland, M., Welsh, J. Thomas. and Sorge, J.A.

TITLE Arbitrarily primed polymerase chain reaction method for fingerprinting genomes

JOURNAL Patent: US 5861245-A 11 19-JAN-1999;

FEATURES  
Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Qy 1 RRRC 4  
Db 15 RRRC 18

RESULT 66  
AR030187/c

LOCUS AR030187 27 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 11 from patent US 5861245.

ACCESSION AR030187

VERSION AR030187.1 GI:5943401

KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)

AUTHORS McClelland, M., Welsh, J. Thomas. and Sorge, J.A.

TITLE Arbitrarily primed polymerase chain reaction method for fingerprinting genomes

JOURNAL Patent: US 5861245-A 11 19-JAN-1999;

FEATURES  
Location/Qualifiers  
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/mol\_type="unassigned DNA"

[illegible]

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/mol_type="unassigned DNA"

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 15 RRC 18

RESULT 72
LOCUS AR477281/c
DEFINITION Sequence 9 from patent US 5487985.
ACCESSION AR477281
VERSION I17359
KEYWORDS I17359.1 GI:1252267
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS McClelland,M., Welsh,J.T. and Sorge,J.A.
TITLE Arbitrarily primed polymerase chain reaction method for
fingerprinting genomes
JOURNAL Patent: US 5487985-A 9 30-JAN-1996;
FEATURES Location/Qualifiers
source 1..27
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ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 10
Db 18 GYY 15

RESULT 73
LOCUS AR477281
DEFINITION Sequence 8 from patent US 6696277.
ACCESSION AR477281
VERSION AR477281.1 GI:47234616
KEYWORDS .
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS McClelland,M., Welsh,J.T. and Sorge,J.A.
TITLE Arbitrarily primed polymerase chain reaction method for
fingerprinting genomes
JOURNAL Patent: US 6696277-A 8 24-FEB-2004;
FEATURES Location/Qualifiers
source 1..27
/mol_type="unknown"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 15 RRC 18

RESULT 74
LOCUS AR477281/c
DEFINITION Sequence 8 from patent US 6696277.
ACCESSION AR477281
VERSION AR477281.1 GI:47234616
KEYWORDS .
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS McClelland,M., Welsh,J.T. and Sorge,J.A.
TITLE Arbitrarily primed polymerase chain reaction method for
fingerprinting genomes
JOURNAL Patent: US 6696277-A 8 24-FEB-2004;
FEATURES Location/Qualifiers
source 1..27
/mol_type="unknown"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 10
Db 18 GYY 15

RESULT 75
LOCUS AR477282
DEFINITION Sequence 9 from patent US 6696277.
ACCESSION AR477282
VERSION AR477282.1 GI:47234617
KEYWORDS .
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS McClelland,M., Welsh,J.T. and Sorge,J.A.
TITLE Arbitrarily primed polymerase chain reaction method for
fingerprinting genomes
JOURNAL Patent: US 6696277-A 9 24-FEB-2004;
FEATURES Location/Qualifiers
source 1..27
/mol_type="unknown"

ORIGIN
Query Match          40.0%; Score 4; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 15 RRC 18

RESULT 76
LOCUS AR477282/c
DEFINITION Sequence 9 from patent US 6696277.
ACCESSION AR477282
VERSION AR477282.1 GI:47234617
KEYWORDS .
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS McClelland,M., Welsh,J.T. and Sorge,J.A.
TITLE Arbitrarily primed polymerase chain reaction method for
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fingerprinting genomes
JOURNAL Patent: US 6696277-A 9 24-FEB-2004;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
Db 18 GYYY 15

RESULT 77
BD132388
LOCUS DNA diagnosis method based on mass spectrometry.
DEFINITION 38 bp DNA linear PAT 18-SEP-2002
ACCESSION BD132388
VERSION BD132388.1 GI:23227333
KEYWORDS JP 2002507883-A/320.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Koester,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
DNA diagnosis method based on mass spectrometry
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 320 12-MAR-2002;
SEQUENCE SEQUNOM INC
PN JP 2002507883-A/320
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR
06-NOV-1996 US 08/746055,06-NOV-1996 US 08/744590 PR
23-JAN-1997 US 08/786988,23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792,08-OCT-1997 US 08/947801 PI HUBERT
KOESTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI GUOBIING
XIANG,
PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
C12Q1/68,C07H21/00,C07F9/24
CC Strandedness: Single;
FH Key Location/Qualifiers
source 1..38
/organism="synthetic construct"
/db_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7
Db 36 CWG 33

RESULT 79
AX328823
LOCUS Sequence 320 from Patent EP1164203.
DEFINITION AX328823 42 bp DNA linear PAT 08-JAN-2002
ACCESSION AX328823
VERSION AX328823.1 GI:18102022
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
DNA diagnostics based on mass spectrometry
TITLE Patent: EP 1164203-A 320 19-DEC-2001;
JOURNAL SEQUNOM, INC. (US)
FEATURES Location/Qualifiers
source 1..42
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 40.0%; Score 4; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7
Db 33 CWG 36

RESULT 80
AX328823/c
LOCUS Sequence 320 from Patent EP1164203.
DEFINITION AX328823
ACCESSION AX328823

```



HHEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)

## FEATURES

source  
 1. .6  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
 ||||  
 Db 3 GY 1

## RESULT 85

E64767 LOCUS 6 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Chemically synthesized artificial promoter for realizing high-level expression of introduced gene and method for synthesizing the same.

ACCESSION E64767  
 VERSION E64767.1 GI:18628530  
 KEYWORDS JP 2000139477-A/8.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 6)  
 AUTHORS Tori, R., Sawanto, S.B., Syngae, P.K. and Guputa, S.K.  
 TITLE Chemically synthesized artificial promoter for realizing high-level expression of introduced gene and method for synthesizing the same  
 JOURNAL Patent: JP 2000139477-A 8 23-MAY-2000;  
 COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH

COMMENT OS Artificial Sequence  
 PN JP 2000139477-A/8  
 PD 23-MAY-2000  
 PF 27-APR-1999 JP 1999119227  
 PR 09-NOV-1998 IN 3322/98  
 PI RAKESH TORI, SALLY BISHWANATO SAWANTO, PURAJUNNA KUMAR SYNGE,  
 SHIFU KUMAR GUPUTA  
 PC C12N15/09, C12N5/10, C12N15/00, C12N5/00  
 CC

FT Key Location/Qualifiers  
 FT source 1. .6  
 /organism="Artificial Sequence".

## FEATURES

source  
 1. .6  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 6  
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 Db 1 CW 3

## RESULT 86

E64767/c LOCUS 6 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Chemically synthesized artificial promoter for realizing high-level expression of introduced gene and method for synthesizing the same.

ACCESSION E64767  
 VERSION E64767.1 GI:18628530  
 KEYWORDS JP 2000139477-A/8.  
 SOURCE synthetic construct

## ORGANISM

synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 6)  
 AUTHORS Tori, R., Sawanto, S.B., Syngae, P.K. and Guputa, S.K.  
 TITLE Chemically synthesized artificial promoter for realizing high-level expression of introduced gene and method for synthesizing the same  
 JOURNAL Patent: JP 2000139477-A 8 23-MAY-2000;  
 COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH

COMMENT OS Artificial Sequence  
 PN JP 2000139477-A/8  
 PD 23-MAY-2000  
 PF 27-APR-1999 JP 1999119227  
 PR 09-NOV-1998 IN 3322/98  
 PI RAKESH TORI, SALLY BISHWANATO SAWANTO, PURAJUNNA KUMAR SYNGE,  
 SHIFU KUMAR GUPUTA  
 PC C12N15/09, C12N5/10, C12N15/00, C12N5/00  
 CC

FT Key Location/Qualifiers  
 FT source 1. .6  
 /organism="Artificial Sequence".

## FEATURES

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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WW 7  
 ||||  
 Db 6 WW 4

## RESULT 87

AX797664 LOCUS 6 bp DNA linear PAT 08-OCT-2003  
 DEFINITION Sequence 27 from Patent WO03039595.  
 ACCESSION AX797664  
 VERSION AX797664.1 GI:37518092

KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Semple, S., Klimuk, S. and Yuan, Z.N.  
 TITLE Mucosal adjuvants comprising an oligonucleotide and a cationic lipid  
 JOURNAL Patent: WO 03039595-A 27 15-MAY-2003;  
 Inex Pharmaceuticals Corp. (CA)

## FEATURES

source  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
 ||||  
 Db 1 RRC 3

## RESULT 88

AX797664/c LOCUS 6 bp DNA linear PAT 08-OCT-2003  
 DEFINITION Sequence 27 from Patent WO03039595.  
 ACCESSION AX797664

VERSION AX977664.1 GI:37518092  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Semple,S., Klimuk,S. and Yuan,Z.N.  
TITLE Mucosal adjuvants comprising an oligonucleotide and a cationic lipid  
JOURNAL Patent: WO 03039595-A 27 15-MAY-2003;  
Inex Pharmaceuticals Corp. (CA)  
FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 RRC 4  
Db 6 RRC 4  
RESULT 89  
LOCUS AX957648 6 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 27 from Patent WO03094963.  
ACCESSION AX957648  
VERSION AX957648.1 GI:40785520  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.  
TITLE Methylated immunostimulatory oligonucleotides and methods of using the same  
JOURNAL Patent: WO 03094963-A 27 20-NOV-2003;  
Inex Pharmaceuticals Corporation (CA)  
FEATURES  
source  
1. .6  
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/db\_xref="taxon:32630"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 RRC 4  
Db 1 RRC 3  
RESULT 90  
LOCUS AX957648/c 6 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 27 from Patent WO03094963.  
ACCESSION AX957648  
VERSION AX957648.1 GI:40785520  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.  
TITLE Methylated immunostimulatory oligonucleotides and methods of using

the same  
JOURNAL Patent: WO 03094963-A 27 20-NOV-2003;  
Inex Pharmaceuticals Corporation (CA)  
FEATURES  
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/db\_xref="taxon:32630"  
/note="synthetic"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 RRC 4  
Db 6 RRC 4  
RESULT 91  
LOCUS AX957742 6 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 27 from Patent WO03094828.  
ACCESSION AX957742  
VERSION AX957742.1 GI:40785560  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.  
TITLE Cancer vaccines and methods of using the same  
JOURNAL Patent: WO 03094828-A 27 20-NOV-2003;  
Inex Pharmaceuticals Corp. (CA)  
FEATURES  
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/db\_xref="taxon:32630"  
/note="synthetic"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 RRC 4  
Db 1 RRC 3  
RESULT 92  
LOCUS AX957742/c 6 bp DNA linear PAT 08-JAN-2004  
DEFINITION Sequence 27 from Patent WO03094828.  
ACCESSION AX957742  
VERSION AX957742.1 GI:40785560  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.  
TITLE Cancer vaccines and methods of using the same  
JOURNAL Patent: WO 03094828-A 27 20-NOV-2003;  
Inex Pharmaceuticals Corp. (CA)  
FEATURES  
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/db\_xref="taxon:32630"  
/note="synthetic"



## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
 |||  
 Db 6 RRC 4

RESULT 93  
 AX958147  
 LOCUS AX958147 6 bp DNA linear PAT 08-JAN-2004  
 DEFINITION Sequence 27 from Patent WO03094829.  
 ACCESSION AX958147  
 VERSION AX958147.1 GI:40785811  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Sample,S., Chikh,G., Hope,M.J. and Tam,Y.K.  
 TITLE Pathogen vaccines and methods for using the same  
 JOURNAL Patent: WO 03094829-A 27 20-NOV-2003;  
 Inex Pharmaceuticals Corp. (CA)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="synthetic"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 2 RRC 4  
 |||  
 Db 1 RRC 3

RESULT 94  
 AX958147/c  
 LOCUS AX958147 6 bp DNA linear PAT 08-JAN-2004  
 DEFINITION Sequence 27 from Patent WO03094829.  
 ACCESSION AX958147  
 VERSION AX958147.1 GI:40785811  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Sample,S., Chikh,G., Hope,M.J. and Tam,Y.K.  
 TITLE Pathogen vaccines and methods for using the same  
 JOURNAL Patent: WO 03094829-A 27 20-NOV-2003;  
 Inex Pharmaceuticals Corp. (CA)  
 FEATURES Location/Qualifiers  
 source 1..6  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="synthetic"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
 |||  
 Db 6 RRC 4

## RESULT 95

BD211369  
 LOCUS BD211369 7 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Method of finding restriction enzyme.  
 ACCESSION BD211369  
 VERSION BD211369.1 GI:33021139  
 KEYWORDS JP 2002517260-A/93.  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 7)  
 AUTHORS Raleigh,E.A., Vaisvila,R. and Morgan,R.D.  
 TITLE Method of finding restriction enzyme  
 JOURNAL Patent: JP 2002517260-A 93 18-JUN-2002;  
 NEW ENGLAND BIOLABS INC  
 COMMENT OS Unknown  
 PN JP 2002517260-A/93  
 PD 18-JUN-2002  
 PF 11-JUN-1999 JP 2000553622  
 PR 12-JUN-1998 US 60/089086,12-JUN-1998 US 60/089101 PI  
 ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC  
 C12Q1/68,C12N15/09,C12N15/00  
 CC Description of Unknown Organism: Consensus sequence CC  
 Position 4, 5 & 6 - R = A or G; Position 7 - Y = C or T FH Key  
 Location/Qualifiers  
 source 1..7  
 FT source  
 FT /organism='Unknown'.  
 Location/Qualifiers  
 1..7  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

## FEATURES

source

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
 |||  
 Db 4 RRR 6

## RESULT 96

BD211369/c  
 LOCUS BD211369 7 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Method of finding restriction enzyme.  
 ACCESSION BD211369  
 VERSION BD211369.1 GI:33021139  
 KEYWORDS JP 2002517260-A/93.  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 7)  
 AUTHORS Raleigh,E.A., Vaisvila,R. and Morgan,R.D.  
 TITLE Method of finding restriction enzyme  
 JOURNAL Patent: JP 2002517260-A 93 18-JUN-2002;  
 NEW ENGLAND BIOLABS INC  
 COMMENT OS Unknown  
 PN JP 2002517260-A/93  
 PD 18-JUN-2002  
 PF 11-JUN-1999 JP 2000553622  
 PR 12-JUN-1998 US 60/089086,12-JUN-1998 US 60/089101 PI  
 ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC  
 C12Q1/68,C12N15/09,C12N15/00  
 CC Description of Unknown Organism: Consensus sequence CC  
 Position 4, 5 & 6 - R = A or G; Position 7 - Y = C or T FH Key  
 Location/Qualifiers  
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 FT source  
 FT /organism='Unknown'.  
 Location/Qualifiers

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Location/Qualifiers

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/db_xref="taxon:32644"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
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Db 6 YYY 4

RESULT 97
BD211370
LOCUS      7 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of finding restriction enzyme.
ACCESSION  BD211370
VERSION     BD211370.1 GI:33021140
KEYWORDS   JP 2002517260-A/94.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 7)
AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
TITLE     Method of finding restriction enzyme
JOURNAL   Patent: JP 2002517260-A 94 18-JUN-2002;
          NEW ENGLAND BIOLABS INC
COMMENT   OS Unknown
          PN JP 2002517260-A/94
          PD 18-JUN-2002
          PF 11-JUN-1999 JP 2000553622
          PR 12-JUN-1998 US 60/089086,12-JUN-1998 US 60/089101 PI
          ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
          C12Q1/68,C12N15/09,C12N15/00
          CC Description of Unknown Organism: Consensus sequence CC
          Position 1 - R = A or G; Position 2, 3 & 4 - Y = C or T FH Key
          FT source 1..7
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             Location/Qualifiers
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ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
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Db 4 RRR 2

RESULT 99
E64766
LOCUS      8 bp DNA linear PAT 31-JAN-2002
DEFINITION Chemically synthesized artificial promoter for realizing high-level
          expression of introduced gene and method for synthesizing the
          same.
ACCESSION  E64766
VERSION     E64766.1 GI:18628529
KEYWORDS   JP 2000139477-A/7.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Tori,R., Sawanto,S.B., Synge,P.K. and Gupta,S.K.
TITLE     Chemically synthesized artificial promoter for realizing high-level
          expression of introduced gene and method for synthesizing the same
          Patent: JP 2000139477-A 7 23-MAY-2000;
          COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
COMMENT   OS Artificial Sequence
          PN JP 2000139477-A/7
          PD 23-MAY-2000
          PF 27-APR-1999 JP 1999119227
          PR 09-NOV-1998 IN 3322/98
          PI RAKESH TORI,SALLY BISHWANATO SAWANTO,PURAJUNNA KUMAR SYNGE,
          PI SHIFU KUNAR GUPUTA
          PC C12N15/09,C12N5/10,C12N15/00,C12N5/00
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          FH Key Location/Qualifiers
          FT source 1..8
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             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
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Db 1 RRR 3

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/organism="unidentified"
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ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
    |||
Db 2 YYY 4

RESULT 98
BD211370/c
LOCUS      7 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of finding restriction enzyme.
ACCESSION  BD211370
VERSION     BD211370.1 GI:33021140
KEYWORDS   JP 2002517260-A/94.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 7)
AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
TITLE     Method of finding restriction enzyme
JOURNAL   Patent: JP 2002517260-A 94 18-JUN-2002;
          NEW ENGLAND BIOLABS INC

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RESULT 100
E64766/c
LOCUS      8 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION  Chemically synthesized artificial promoter for realizing high-level
              expression of introduced gene and method for synthesizing the
              same.
ACCESSION  E64766
VERSION    E64766.1  GI:18628529
KEYWORDS   JP 2000139477-A/7.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Tori,R.; Sawanto,S.B., Syngae,P.K. and Gupta,S.K.
TITLE      Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the same
JOURNAL    Patent: JP 2000139477-A 7 23-MAY-2000;
COMMENT    COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
           PN JP 2000139477-A/7
           PD 23-MAY-2000
           PP 27-APR-1999 JP 1999119227
           PR 09-NOV-1998 IN 3222/98
           PI RAKESH TORI,SALLY BISHWANATO SAWANTO,PURAJUNNA KUMAR SYNGAE,
           PC SHIFU KOMAR GUPTA
           CC C12N15/09,C12N5/10,C12N15/00,C12N5/00
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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
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Db 8 YYY 6

RESULT 101
AX046162
LOCUS      8 bp      DNA      linear      PAT 24-NOV-2000
DEFINITION  Sequence 41 from Patent WO0066734.
ACCESSION  AX046162
VERSION    AX046162.1  GI:11344245
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Lee,M.E. and Yet,S.F.
TITLE      Methods of treating hypertension
JOURNAL    Patent: WO 0066734-A 41 09-NOV-2000;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
COMMENT    COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
           PN JP 2000139477-A/7
           PD 23-MAY-2000
           PP 27-APR-1999 JP 1999119227
           PR 09-NOV-1998 IN 3222/98
           PI RAKESH TORI,SALLY BISHWANATO SAWANTO,PURAJUNNA KUMAR SYNGAE,
           PC SHIFU KOMAR GUPTA
           CC C12N15/09,C12N5/10,C12N15/00,C12N5/00
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FEATURES   source
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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
   |||
Db 8 YYY 6

RESULT 102
AX046162/c
LOCUS      8 bp      DNA      linear      PAT 24-NOV-2000
DEFINITION  Sequence 41 from Patent WO0066734.
ACCESSION  AX046162
VERSION    AX046162.1  GI:11344245
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Lee,M.E. and Yet,S.F.
TITLE      Methods of treating hypertension
JOURNAL    Patent: WO 0066734-A 41 09-NOV-2000;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
COMMENT    COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
           PN JP 2000139477-A/7
           PD 23-MAY-2000
           PP 27-APR-1999 JP 1999119227
           PR 09-NOV-1998 IN 3222/98
           PI RAKESH TORI,SALLY BISHWANATO SAWANTO,PURAJUNNA KUMAR SYNGAE,
           PC SHIFU KOMAR GUPTA
           CC C12N15/09,C12N5/10,C12N15/00,C12N5/00
           FH Key
           FT Location/Qualifiers
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           FT /mol_type='genomic DNA'
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FEATURES   source
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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
   |||
Db 8 YYY 6

RESULT 103
BD084758
LOCUS      8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION  Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION  BD084758
VERSION    BD084758.1  GI:22630368
KEYWORDS   JP 2001521375-A/56.
SOURCE     unidentified
            unidentified
            unclassified.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
TITLE      Human nerve growth factor exon 1 and exon 3 promoters
JOURNAL    Patent: JP 2001521375-A 56 06-NOV-2001;
            HOECHST MARION ROUSSEL INC
COMMENT    OS Unidentified
           PN JP 2001521375-A/56
           PD 06-NOV-2001
           PP 12-JAN-1998 JP 1998534446
           PR 06-FEB-1997 US 60/038212
           PI MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN PI
             SUBRAMANIAM
           PC C07K14/48,C12Q1/68
           CC Strandedness: Double;
           CC Topology: Unknown;
           CC Human nerve growth factor exon 1 and exon 3 promoters FH Key
FEATURES   source
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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
   |||
Db 8 YYY 6

RESULT 104
AX046162
LOCUS      8 bp      DNA      linear      PAT 24-NOV-2000
DEFINITION  Sequence 41 from Patent WO0066734.
ACCESSION  AX046162
VERSION    AX046162.1  GI:11344245
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Lee,M.E. and Yet,S.F.
TITLE      Methods of treating hypertension
JOURNAL    Patent: WO 0066734-A 41 09-NOV-2000;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
COMMENT    COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
           PN JP 2000139477-A/7
           PD 23-MAY-2000
           PP 27-APR-1999 JP 1999119227
           PR 09-NOV-1998 IN 3222/98
           PI RAKESH TORI,SALLY BISHWANATO SAWANTO,PURAJUNNA KUMAR SYNGAE,
           PC SHIFU KOMAR GUPTA
           CC C12N15/09,C12N5/10,C12N15/00,C12N5/00
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FEATURES   source
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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
   |||
Db 8 YYY 6

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Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
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Db      6 WWG 8

RESULT 104
BD084758/c
LOCUS      BD084758      8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION  BD084758
VERSION     BD084758.1 GI:22630368
KEYWORDS   JP 2001521375-A/56.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
TITLE     Human nerve growth factor exon 1 and exon 3 promoters
JOURNAL   Patent: JP 2001521375-A 56 06-NOV-2001;
          HOECHST MARION ROUSSEL INC
COMMENT   OS Unidentified
          FN JP 2001521375-A/56
          PD 06-NOV-2001
          PF 12-JAN-1998 JP 1998534446
          PR 06-FEB-1997 US 60/038212
          PI MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN PI
          SUBRAMANIAM
          PC C07K14/48,C12Q1/68
          CC Strandedness: Double;
          CC Topology: Unknown;
          CC Human nerve growth factor exon 1 and exon 3 promoters FH Key
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Query Match      30.0%; Score 3; DB 6; Length 8;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
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Db      8 CWW 6

RESULT 105
A37861
LOCUS      A37861      10 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 4 from Patent WO9408025.
ACCESSION  A37861
VERSION     A37861.1 GI:2294541
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
          EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
JOURNAL   Patent: WO 9408025-A 4 14-APR-1994;
          INST NAT SANTE RECH MED (FR)
          Other publication FR 2696181 940401.
COMMENT   Location/Qualifiers
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ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
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Db      1 YYY 3

RESULT 106
A37861/c
LOCUS      A37861      10 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 4 from Patent WO9408025.
ACCESSION  A37861
VERSION     A37861.1 GI:2294541
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
          EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
JOURNAL   Patent: WO 9408025-A 4 14-APR-1994;
          INST NAT SANTE RECH MED (FR)
          Other publication FR 2696181 940401.
COMMENT   Location/Qualifiers
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ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
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Db      1 YYY 3

RESULT 107
AR074451
LOCUS      AR074451      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 23 from patent US 5955075.
ACCESSION  AR074451
VERSION     AR074451.1 GI:10001206
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL   Patent: US 5955075-A 23 21-SEP-1999;
          Location/Qualifiers
FEATURES
source
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Location/Qualifiers
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ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10

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source
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ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      1 YYY 3

RESULT 106
A37861/c
LOCUS      A37861      10 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 4 from Patent WO9408025.
ACCESSION  A37861
VERSION     A37861.1 GI:2294541
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
          EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
JOURNAL   Patent: WO 9408025-A 4 14-APR-1994;
          INST NAT SANTE RECH MED (FR)
          Other publication FR 2696181 940401.
COMMENT   Location/Qualifiers
FEATURES
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Location/Qualifiers
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ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
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Db      3 RRR 1

RESULT 107
AR074451
LOCUS      AR074451      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 23 from patent US 5955075.
ACCESSION  AR074451
VERSION     AR074451.1 GI:10001206
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL   Patent: US 5955075-A 23 21-SEP-1999;
          Location/Qualifiers
FEATURES
source
1..10
Location/Qualifiers
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/mol_type='unassigned DNA'

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10

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Db 1 YYY 3  
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RESULT 108  
AR074451/c LOCUS 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 23 from patent US 5955075.  
ACCESSION AR074451  
VERSION AR074451.1 GI:10001206  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 23 21-SEP-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
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Db 10 RRR 8  
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RESULT 109  
AR081131 LOCUS 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 23 from patent US 5972353.  
ACCESSION AR081131  
VERSION AR081131.1 GI:10007859  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 23 26-OCT-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
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Db 10 RRR 8  
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RESULT 110  
AR081131/c LOCUS 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 23 from patent US 5972353.  
ACCESSION AR081131  
VERSION AR081131.1 GI:10007859  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 23 26-OCT-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
|||  
Db 1 YYY 3  
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AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 23 26-OCT-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
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Db 10 RRR 8  
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RESULT 111  
AR085328 LOCUS 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 23 from patent US 5981711.  
ACCESSION AR085328  
VERSION AR085328.1 GI:10012097  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 23 09-NOV-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 YYY 10  
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Db 1 YYY 3  
|||  
RESULT 112  
AR085328/c LOCUS 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 23 from patent US 5981711.  
ACCESSION AR085328  
VERSION AR085328.1 GI:10012097  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 23 09-NOV-1999;  
FEATURES Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
|||

```
Db          10 RRR 8

RESULT 113
LOCUS      AR088076
DEFINITION Sequence 23 from patent US 5989838.
ACCESSION  AR088076
VERSION     AR088076.1 GI:10014839
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL   Patent: US 5989838-A 23 23-NOV-1999;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
        |||
        1 YYY 3

Db

RESULT 114
LOCUS      AR088076/c
DEFINITION Sequence 23 from patent US 5989838.
ACCESSION  AR088076
VERSION     AR088076.1 GI:10014839
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Detection and quantitation of MN-specific antibodies
JOURNAL   Patent: US 5989838-A 23 23-JUL-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
        |||
        1 YYY 3

Db

RESULT 115
LOCUS      AR104235
DEFINITION Sequence 23 from patent US 6093548.
ACCESSION  AR104235
VERSION     AR104235.1 GI:12816943
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Detection and quantitation of MN-specific antibodies
JOURNAL   Patent: US 6093548-A 23 25-JUL-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
        |||
        10 RRR 8

Db

RESULT 116
LOCUS      AR104235/c
DEFINITION Sequence 23 from patent US 6093548.
ACCESSION  AR104235
VERSION     AR104235.1 GI:12816943
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     Detection and quantitation of MN-specific antibodies
JOURNAL   Patent: US 6093548-A 23 25-JUL-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
        |||
        1 YYY 3

Db

RESULT 117
LOCUS      AR110243
DEFINITION Sequence 47 from patent US 6114311.
ACCESSION  AR110243
VERSION     AR110243.1 GI:12826519
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Parmacek,M.S. and Solway,J.
TITLE     Method for modulating smooth muscle cell proliferation
JOURNAL   Patent: US 6114311-A 47 05-SEP-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
        |||
        2 CWW 4
```

```
RESULT 118
ARI10243/c
LOCUS           ARI10243           10 bp    DNA
DEFINITION      Sequence 47 from patent US 6114311.
ACCESSION       ARI10243
VERSION         ARI10243.1  GI:12826519
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Parmacek,M.S. and Solway,J.
TITLE          Method for modulating smooth muscle cell proliferation
JOURNAL        Patent: US 6114311-A 47 05-SEP-2000;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              5 WVG 7
                |||
Db              4 WVG 2

RESULT 119
ARI134895
LOCUS           ARI134895           10 bp    DNA
DEFINITION      Sequence 11 from patent US 6194211.
ACCESSION       ARI134895
VERSION         ARI134895.1  GI:14123800
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Richards,C.Ann. and Huber,B.
TITLE          Transcriptional regulatory sequence of carcinoembryonic antigen for
                expression targeting
JOURNAL        Patent: US 6194211-A 11 27-FEB-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              4 CWV 6
                |||
Db              2 CWV 4

RESULT 120
ARI134895/c
LOCUS           ARI134895           10 bp    DNA
DEFINITION      Sequence 11 from patent US 6194211.
ACCESSION       ARI134895
VERSION         ARI134895.1  GI:14123800
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Richards,C.Ann. and Huber,B.
TITLE          Transcriptional regulatory sequence of carcinoembryonic antigen for
                expression targeting
JOURNAL        Patent: US 6194211-A 11 27-FEB-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              4 CWV 6
                |||
Db              2 CWV 4

RESULT 121
ARI139421
LOCUS           ARI139421           10 bp    DNA
DEFINITION      Sequence 1 from patent US 6207377.
ACCESSION       ARI139421
VERSION         ARI139421.1  GI:14481917
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Wayne,J. and Xu,S.-y.
TITLE          Method for construction of thermus-E. coli shuttle vectors and
                identification of two Thermus plasmid replication origins
JOURNAL        Patent: US 6207377-A 1 27-MAR-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              2 RRC 4
                |||
Db              1 RRC 3

RESULT 122
ARI139421/c
LOCUS           ARI139421           10 bp    DNA
DEFINITION      Sequence 1 from patent US 6207377.
ACCESSION       ARI139421
VERSION         ARI139421.1  GI:14481917
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Wayne,J. and Xu,S.-y.
TITLE          Method for construction of thermus-E. coli shuttle vectors and
                identification of two Thermus plasmid replication origins
JOURNAL        Patent: US 6207377-A 1 27-MAR-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              2 RRC 4
                |||
Db              1 RRC 3

TITLE          Transcriptional regulatory sequence of carcinoembryonic antigen for
                expression targeting
JOURNAL        Patent: US 6194211-A 11 27-FEB-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              4 CWV 6
                |||
Db              2 CWV 4

RESULT 120
ARI134895/c
LOCUS           ARI134895           10 bp    DNA
DEFINITION      Sequence 11 from patent US 6194211.
ACCESSION       ARI134895
VERSION         ARI134895.1  GI:14123800
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 10)
AUTHORS        Richards,C.Ann. and Huber,B.
TITLE          Transcriptional regulatory sequence of carcinoembryonic antigen for
                expression targeting
JOURNAL        Patent: US 6194211-A 11 27-FEB-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              4 CWV 6
                |||
Db              2 CWV 4

TITLE          Transcriptional regulatory sequence of carcinoembryonic antigen for
                expression targeting
JOURNAL        Patent: US 6194211-A 11 27-FEB-2001;
FEATURES        Location/Qualifiers
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              4 CWV 6
                |||
Db              2 CWV 4
```

Qy 1 RRR 3  
Db 10 RRR 8

RESULT 123  
AR143499  
LOCUS AR143499 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 23 from patent US 6204370.  
ACCESSION AR143499  
VERSION AR143499.1 GI:15104785  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6204370-A 23 20-MAR-2001;  
FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

RESULT 124  
AR143499/c  
LOCUS AR143499/c 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 23 from patent US 6204370.  
ACCESSION AR143499  
VERSION AR143499.1 GI:15104785  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6204370-A 23 20-MAR-2001;  
FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

RESULT 125  
AR170002  
LOCUS AR170002 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 47 from patent US 6291211.  
ACCESSION AR170002  
VERSION AR170002.1 GI:17907961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Parmacek,M.S. and Solway,J.  
TITLE Promoter for smooth muscle cell expression  
JOURNAL Patent: US 6291211-A 47 18-SEP-2001;  
FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
Db 2 CWW 4

RESULT 126  
AR170002/c  
LOCUS AR170002/c 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 47 from patent US 6291211.  
ACCESSION AR170002  
VERSION AR170002.1 GI:17907961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Parmacek,M.S. and Solway,J.  
TITLE Promoter for smooth muscle cell expression  
JOURNAL Patent: US 6291211-A 47 18-SEP-2001;  
FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7  
Db 4 WWG 2

RESULT 127  
AR171403  
LOCUS AR171403 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 23 from patent US 6297041.  
ACCESSION AR171403  
VERSION AR171403.1 GI:17910353  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6297041-A 23 02-OCT-2001;  
FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10



```
Db      |||
1 YYY 3

RESULT 128
LOCUS   AR171403/c          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 23 from patent US 6297041.
ACCESSION   AR171403
VERSION     AR171403.1   GI:17910353
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN gene and protein
JOURNAL    Patent: US 6297041-A 23 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
        |||
Db      10 RRR 8

RESULT 129
LOCUS   AR171574          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 23 from patent US 6297051.
ACCESSION   AR171574
VERSION     AR171574.1   GI:17910524
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN gene and protein
JOURNAL    Patent: US 6297051-A 23 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
        |||
Db      10 RRR 8

RESULT 130
LOCUS   AR171574/c          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 23 from patent US 6297051.
ACCESSION   AR171574
VERSION     AR171574.1   GI:17910524
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN gene and protein
JOURNAL    Patent: US 6297051-A 23 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
        |||
Db      1 YYY 3

RESULT 131
LOCUS   AR171811          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 47 from patent US 6297221.
ACCESSION   AR171811
VERSION     AR171811.1   GI:17910761
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Farmacek,M.S. and Solway,J.
TITLE      Method for promoting angiogenesis with a nucleic acid construct
            comprising an SM22.alpha.0 promoter
JOURNAL    Patent: US 6297221-A 47 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
        |||
Db      2 CWW 4

RESULT 132
LOCUS   AR171811/c          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 47 from patent US 6297221.
ACCESSION   AR171811
VERSION     AR171811.1   GI:17910761
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Farmacek,M.S. and Solway,J.
TITLE      Method for promoting angiogenesis with a nucleic acid construct
            comprising an SM22.alpha.0 promoter
JOURNAL    Patent: US 6297221-A 47 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
        |||
Db      1 YYY 3

RESULT 133
LOCUS   AR171574/c          10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION   Sequence 23 from patent US 6297051.
ACCESSION   AR171574
VERSION     AR171574.1   GI:17910524
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN gene and protein
JOURNAL    Patent: US 6297051-A 23 02-OCT-2001;
FEATURES   Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
        |||
Db      10 RRR 8
```

```

QY      5 WWG 7
Db      4 WWG 2

RESULT 133
LOCUS   BD189505
DEFINITION PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION.
ACCESSION BD189505
VERSION   BD189505.1 GI:32999244
KEYWORDS  JP 2003009894-A/38.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Parmacek,M.S. and Solway,J.
TITLE     PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
JOURNAL   Patent: JP 2003009894-A 38 14-JAN-2003;
COMMENT   ARCH DEVELOPMENT CORPORATION
OS        Artificial Sequence
PN        JP 2003009894-A/38
PD        14-JAN-2003
PF        10-MAY-2002 JP 2002136310
PR        07-OCT-1996 US 08/726807
PI        michael s parmacek,julian solway
CC        Description of Artificial Sequence: PRIMER
FH        Key Location/Qualifiers.
FEATURES             source
1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWG 6
Db      2 CWG 4

RESULT 134
LOCUS   BD189505/c
DEFINITION PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION.
ACCESSION BD189505
VERSION   BD189505.1 GI:32999244
KEYWORDS  JP 2003009894-A/38.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Parmacek,M.S. and Solway,J.
TITLE     PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
JOURNAL   Patent: JP 2003009894-A 38 14-JAN-2003;
COMMENT   ARCH DEVELOPMENT CORPORATION
OS        Artificial Sequence
PN        JP 2003009894-A/38
PD        14-JAN-2003
PF        10-MAY-2002 JP 2002136310
PR        07-OCT-1996 US 08/726807
PI        michael s parmacek,julian solway
CC        Description of Artificial Sequence: PRIMER
FH        Key Location/Qualifiers.
FEATURES             source
1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
Db      4 WWG 2

RESULT 135
LOCUS   BD243164
DEFINITION MN gene and protein.
ACCESSION BD243164
VERSION   BD243164.1 GI:33052934
KEYWORDS  JP 2002528085-A/13.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN gene and protein
JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
COMMENT   INSTITUTE OF VIROLOGY
OS        Homo sapiens (human)
PN        JP 2002528085-A/13
PD        03-SEP-2002
PF        22-OCT-1999 JP 2000578455
PR        23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
PI        JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
CC        C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
FH        C07K14/47,
PC        C1201/02,G01N33/566/(C12Q1/02,C12R1/91),C12N15/00,A61K37/02
CC        MN gene and protein
FH        Key Location/Qualifiers
FT        misc feature (1)..(10).
            Location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      1 YYY 3

RESULT 136
LOCUS   BD243164/c
DEFINITION MN gene and protein.
ACCESSION BD243164
VERSION   BD243164.1 GI:33052934
KEYWORDS  JP 2002528085-A/13.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN gene and protein
JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
COMMENT   INSTITUTE OF VIROLOGY
OS        Homo sapiens (human)
PN        JP 2002528085-A/13
PD        03-SEP-2002

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Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
Db      4 WWG 2

RESULT 135
LOCUS   BD243164
DEFINITION MN gene and protein.
ACCESSION BD243164
VERSION   BD243164.1 GI:33052934
KEYWORDS  JP 2002528085-A/13.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN gene and protein
JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
COMMENT   INSTITUTE OF VIROLOGY
OS        Homo sapiens (human)
PN        JP 2002528085-A/13
PD        03-SEP-2002
PF        22-OCT-1999 JP 2000578455
PR        23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
PI        JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
CC        C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
FH        C07K14/47,
PC        C1201/02,G01N33/566/(C12Q1/02,C12R1/91),C12N15/00,A61K37/02
CC        MN gene and protein
FH        Key Location/Qualifiers
FT        misc feature (1)..(10).
            Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      1 YYY 3

RESULT 136
LOCUS   BD243164/c
DEFINITION MN gene and protein.
ACCESSION BD243164
VERSION   BD243164.1 GI:33052934
KEYWORDS  JP 2002528085-A/13.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN gene and protein
JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
COMMENT   INSTITUTE OF VIROLOGY
OS        Homo sapiens (human)
PN        JP 2002528085-A/13
PD        03-SEP-2002

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PF 22-OCT-1999 JP 2000578465  
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI  
JAN ZAVADA, SILVIA PASTOREKOVA, JAROMIR PASTOREK PC  
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC  
C07K14/47,  
PC C12Q1/02,G01N33/566/(C12Q1/02,C12R1:91),C12N15/00,A61K37/02  
CC MN gene and protein  
FH Key Location/Qualifiers  
FT misc feature (1)..(10).  
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source  
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Query Match 30.0%; Score 3; DB 6; Length 10;  
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
10 RRR 8  
Db  
RESULT 137  
CQ814915 CQ814915 10 bp DNA linear PAT 24-MAY-2004  
LOCUS  
DEFINITION Sequence 1 from Patent WO2004039980.  
ACCESSION CQ814915  
VERSION CQ814915.1 GI:47604076  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Treisman,R.H., Miralles-Arenas,F., Zaromytidou,A.I. and Posern,G.  
TITLE Agents modulating mal activity  
JOURNAL Patent: WO 2004039980-A 1 13-MAY-2004;  
Cancer Research Technology Limited (GB)  
FEATURES  
source  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWW 6  
2 CWW 4  
Db  
RESULT 138  
CQ814915/c CQ814915 10 bp DNA linear PAT 24-MAY-2004  
LOCUS  
DEFINITION Sequence 1 from Patent WO2004039980.  
ACCESSION CQ814915  
VERSION CQ814915.1 GI:47604076  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Treisman,R.H., Miralles-Arenas,F., Zaromytidou,A.I. and Posern,G.  
TITLE Agents modulating mal activity  
JOURNAL Patent: WO 2004039980-A 1 13-MAY-2004;  
Cancer Research Technology Limited (GB)  
FEATURES  
Location/Qualifiers  
source

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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Consensus sequence of the CarG box"  
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ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWW 6  
9 CWW 7  
Db  
RESULT 139  
I72403 I72403 10 bp DNA linear PAT 03-APR-1998  
LOCUS  
DEFINITION Sequence 34 from patent US 5683985.  
ACCESSION I72403  
VERSION I72403.1 GI:3008542  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chu,B.Chen.Fei. and Orgel,L.  
TITLE Oligonucleotide decoys and methods relating thereto  
JOURNAL Patent: US 5683985-A 34 04-NOV-1997;  
FEATURES  
source  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWW 6  
2 CWW 4  
Db  
RESULT 140  
I72403/c I72403 10 bp DNA linear PAT 03-APR-1998  
LOCUS  
DEFINITION Sequence 34 from patent US 5683985.  
ACCESSION I72403  
VERSION I72403.1 GI:3008542  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chu,B.Chen.Fei. and Orgel,L.  
TITLE Oligonucleotide decoys and methods relating thereto  
JOURNAL Patent: US 5683985-A 34 04-NOV-1997;  
FEATURES  
source  
ORIGIN  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWW 6  
9 CWW 7  
Db

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RESULT 141
LOCUS       I84595
DEFINITION Sequence 1 from patent US 5695977.
ACCESSION   I84595
VERSION     I84595.1 GI:3022115
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Jurka,J.W.
TITLE      Site directed recombination
JOURNAL    Patent: US 5695977-A 1 09-DEC-1997;
FEATURES   Location/Qualifiers
            source
              1..10
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              /mol_type="unassigned DNA"
ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      7 YYY 9

RESULT 142
LOCUS       I84595/c
DEFINITION Sequence 1 from patent US 5695977.
ACCESSION   I84595
VERSION     I84595.1 GI:3022115
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Jurka,J.W.
TITLE      Site directed recombination
JOURNAL    Patent: US 5695977-A 1 09-DEC-1997;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      7 YYY 9

RESULT 143
LOCUS       I84606
DEFINITION Sequence 12 from patent US 5695977.
ACCESSION   I84606
VERSION     I84606.1 GI:3022126
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Jurka,J.W.
TITLE      Site directed recombination
JOURNAL    Patent: US 5695977-A 12 09-DEC-1997;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      9 YYY 7

RESULT 144
LOCUS       I84606/c
DEFINITION Sequence 12 from patent US 5695977.
ACCESSION   I84606
VERSION     I84606.1 GI:3022126
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Jurka,J.W.
TITLE      Site directed recombination
JOURNAL    Patent: US 5695977-A 12 09-DEC-1997;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
      |||
Db      7 RRR 9

RESULT 145
LOCUS       AR220243
DEFINITION Sequence 3 from patent US 6423693.
ACCESSION   AR220243
VERSION     AR220243.1 GI:233224971
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Schwartz,R.J., Draghia-Akli,R., Li,X. and Eastman,E.M.
TITLE      Growth hormone releasing hormone expression system and methods of
            use, including use in animals
JOURNAL    Patent: US 6423693-A 3 23-JUL-2002;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
      |||
Db      2 CWW 4
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RESULT 146
AR220243/c
LOCUS           AR220243       10 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION     Sequence 3 from patent US 6423693.
ACCESSION      AR220243
VERSION       AR220243.1  GI:23324971
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Schwartz,R.J., Draghia-Akli,R., Li,X. and Eastman,E.M.
TITLE         Growth hormone releasing hormone expression system and methods of
              use, including use in animals
JOURNAL       Patent: US 6423693-A 3 23-JUL-2002;
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"
ORIGIN
Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             4 CWW 6
              |||
Db             9 CWW 7

RESULT 147
AR264148
LOCUS           AR264148       10 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION     Sequence 47 from patent US 6331527.
ACCESSION      AR264148
VERSION       AR264148.1  GI:28076219
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Parmacek,M.S. and Solway,J.
TITLE         Promoter smooth muscle cell expression
JOURNAL       Patent: US 6331527-A 47 18-DEC-2001;
FEATURES      Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             4 CWW 6
              |||
Db             2 CWW 4

RESULT 148
AR264148/c
LOCUS           AR264148       10 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION     Sequence 47 from patent US 6331527.
ACCESSION      AR264148
VERSION       AR264148.1  GI:28076219
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Parmacek,M.S. and Solway,J.
TITLE         Promoter smooth muscle cell expression

JOURNAL       Patent: US 6331527-A 47 18-DEC-2001;
FEATURES      Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             4 CWW 6
              |||
Db             2 CWW 4

JOURNAL       Patent: US 6331527-A 47 18-DEC-2001;
FEATURES      Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             5 WWG 7
              |||
Db             8 WWG 10

RESULT 150
AR362282/c
LOCUS           AR362282       10 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION     Sequence 1 from patent US 5164316.
ACCESSION      AR362282
VERSION       AR362282.1  GI:34422165
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS       McPherson,J.C. and Kay,R.
TITLE         DNA construct for enhancing the efficiency of transcription
JOURNAL       Patent: US 5164316-A 1 17-NOV-1992;
FEATURES      Location/Qualifiers
              1..10
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              /mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             5 WWG 7
              |||
Db             8 WWG 10

RESULT 149
AR362282
LOCUS           AR362282       10 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION     Sequence 1 from patent US 5164316.
ACCESSION      AR362282
VERSION       AR362282.1  GI:34422165
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS       McPherson,J.C. and Kay,R.
TITLE         DNA construct for enhancing the efficiency of transcription
JOURNAL       Patent: US 5164316-A 1 17-NOV-1992;
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"
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Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             4 CWW 6
              |||
Db             10 CWW 8

JOURNAL       Patent: US 5164316-A 1 17-NOV-1992;
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"
ORIGIN
Query Match    30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches        3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             4 CWW 6
              |||
Db             10 CWW 8
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RESULT 151
AX412946
LOCUS
DEFINITION
Sequence 710 from Patent WO0222675.
ACCESSION
AX412946
VERSION
AX412946.1 GI:21445404
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1
Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T.
Plant genes, the expression of which are altered by pathogen
infection
Patent: WO 0222675-A 710 21-MAR-2002;
SYNGENTA PARTICIPATIONS AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES
Location/Qualifiers
source
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/db_xref="taxon:3702"
misc_feature
5..6
/notes="w = adenine or thymine"
misc_feature
9
/notes="w = adenine or thymine"
misc_feature
10
/notes="y = cytosine or thymine"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
|||
Db 4 CWV 6

RESULT 152
AX412946/c
LOCUS
DEFINITION
Sequence 710 from Patent WO0222675.
ACCESSION
AX412946
VERSION
AX412946.1 GI:21445404
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1
Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T.
Plant genes, the expression of which are altered by pathogen
infection
Patent: WO 0222675-A 710 21-MAR-2002;
SYNGENTA PARTICIPATIONS AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
Jeffrey L. (US) ; Eulgem, Thomas (US)
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/notes="w = adenine or thymine"
misc_feature
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/notes="w = adenine or thymine"
misc_feature
10
/notes="w = adenine or thymine"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
|||
Db 4 CWV 6

RESULT 153
AX497559
LOCUS
DEFINITION
Sequence 103 from Patent WO0233126.
ACCESSION
AX497559
VERSION
AX497559.1 GI:23342829
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
Grenier, J.K., Marshall, D.J., Prudent, J.R., Richmond, C.S.,
Roesch, E.B., Scherrer, C.W., Sherrill, C.B. and Ptacin, J.L.
Solid support assay systems and methods utilizing non-standard
bases
Patent: WO 0233126-A 103 25-APR-2002;
ERAGEN BIOSCIENCES, INC. (US)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic Oligonucleotides"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9
|||
Db 1 GY 3

RESULT 154
AX497559/c
LOCUS
DEFINITION
Sequence 103 from Patent WO0233126.
ACCESSION
AX497559
VERSION
AX497559.1 GI:23342829
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
Grenier, J.K., Marshall, D.J., Prudent, J.R., Richmond, C.S.,
Roesch, E.B., Scherrer, C.W., Sherrill, C.B. and Ptacin, J.L.
Solid support assay systems and methods utilizing non-standard
bases
Patent: WO 0233126-A 103 25-APR-2002;
ERAGEN BIOSCIENCES, INC. (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
/notes="Synthetic Oligonucleotides"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9
|||
Db 1 GY 3

RESULT 155
AX497559
LOCUS
DEFINITION
Sequence 103 from Patent WO0233126.
ACCESSION
AX497559
VERSION
AX497559.1 GI:23342829
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
Grenier, J.K., Marshall, D.J., Prudent, J.R., Richmond, C.S.,
Roesch, E.B., Scherrer, C.W., Sherrill, C.B. and Ptacin, J.L.
Solid support assay systems and methods utilizing non-standard
bases
Patent: WO 0233126-A 103 25-APR-2002;
ERAGEN BIOSCIENCES, INC. (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic Oligonucleotides"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9
|||
Db 1 GY 3

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
   |||
Db 3 RRC 1

RESULT 155
BD009036
LOCUS
DEFINITION Promoter for smooth muscle cell expression.
ACCESSION BD009036
VERSION BD009036.1 GI:18637409
KEYWORDS JP 2001502899-A/38.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Parmacek,M.S. and Solway,J.
TITLE Promoter for smooth muscle cell expression
JOURNAL Patent: JP 2001502899-A 38 06-MAR-2001;
ARCH DEVELOPMENT CORP
COMMENT OS Unidentified
PN JP 2001502899-A/38
PD 06-MAR-2001
PF 29-AUG-1997 JP 1998517528
PR 07-OCT-1996 US 08/726807
PI MICHAEL S PARMACEK,JULIAN SOLWAY
PC C07K14/47
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT modified base 3..8.
   Location/Qualifiers
   1..10
   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

FEATURES
   source
   location 10 bp DNA linear PAT 31-JAN-2002

ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
   |||
Db 4 WWG 2

RESULT 157
BD063695
LOCUS
DEFINITION Glutathione-S-conjugate transport in plants.
ACCESSION BD063695
VERSION BD063695.1 GI:22609298
KEYWORDS JP 2001504700-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Rea,P.A., Lu,Y.P. and Li,Z.S.
TITLE Glutathione-S-conjugate transport in plants
JOURNAL Patent: JP 2001504700-A 7 10-APR-2001;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
COMMENT PN JP 2001504700-A/7
PD 10-APR-2001
PF 18-NOV-1997 JP 1998523910
PR 18-NOV-1996 US 60/031040.08-OCT-1997 US 60/061328 PI
PHILIP A REA,YU PING LU,ZE SHENG LI
PC A01H5/00,C07K14/415,C07K16/16,C12N1/13,C12N1/21,C12N5/10, PC
C12N15/29.

FEATURES
   source
   location 10 bp DNA linear PAT 27-AUG-2002

ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
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Db 7 WWG 9

RESULT 158
BD063695/c
LOCUS
DEFINITION Glutathione-S-conjugate transport in plants.
ACCESSION BD063695
VERSION BD063695.1 GI:22609298
KEYWORDS JP 2001504700-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Rea,P.A., Lu,Y.P. and Li,Z.S.
TITLE Glutathione-S-conjugate transport in plants
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JOURNAL Patent: JP 2001504700-A 7 10-APR-2001;
COMMENT THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
PD 10-APR-2001
PF 18-NOV-1997 JP 1998523910
PR 18-NOV-1996 US 60/031040, 08-OCT-1997 US 60/061328 PI
PHILIP A. REA, YU PING LU, ZE SHENG LI
PC A01H5/00, C07K14/415, C07K16/16, C12N1/13, C12N1/21, C12N5/10, PC
C12N15/29,
PC C12N15/64, C12N15/82
CC C12N15/09, C12N5/06, C12N5/22, C07K14/60, C12N15/00,
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES source
1. .10 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CW 6
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Db 9 CW 7
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RESULT 159
BD073429
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Expression system of GHRH and utilization method.
ACCESSION BD073429
VERSION BD073429.1 GI:22619032
KEYWORDS JP 2001511353-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Schwartz,R.J., Akli,R.D., Li,X. and Eastman,E.M.
TITLE Expression system of GHRH and utilization method
JOURNAL Patent: JP 2001511353-A 3 14-AUG-2001;
BARENTIS INC
COMMENT OS PSK-GHRH
PN JP 2001511353-A/3
PD 14-AUG-2001
PF 24-JUL-1998 JP 2000504270
PR 24-JUL-1997 US 60/053609, 20-OCT-1997 US 60/062608 PI
ROBERT J SCHWARTZ, RUXANDRA DRAGHIA AKLI, XUYANG LI, ERIC M PI
EASTMAN
PC C12N15/09, A01K67/027, C12N5/10//A61K38/22, C07K14/60, C12N15/00,
PC C12N5/00,
PC A61K37/24
CC The letter 'w' stands for a or t.
FH Key Location/Qualifiers
FT source 1. .10
/organism="PSK-GHRH".
FEATURES source
1. .10 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CW 6
|||
Db 9 CW 7
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RESULT 161
BD091328
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION In vitro differentiation of vascular smooth muscle cells, and
method and reagent related thereto.
ACCESSION BD091328
VERSION BD091328.1 GI:22636938
KEYWORDS JP 2001520877-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lee,A.M.E., Jain,M. and Watanabe,M.
TITLE In vitro differentiation of vascular smooth muscle cells, and
method and reagent related thereto
JOURNAL Patent: JP 2001520877-A 3 06-NOV-2001;
PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT OS Artificial Sequence
PN JP 2001520877-A/3
PD 06-NOV-2001
PF 28-OCT-1998 JP 2000518057
PR 28-OCT-1997 US 60/063363, 02-APR-1998 US 60/080420 PR
14-AUG-1998 US 60/096685
PC ARTHUR M E LEE, MUKESH JAIN, MASAFUMI WATANABE
PC C12N15/09, C12N5/06, C12N15/00, C12N5/00
CC Description of Artificial Sequence: CARG box
FH Key Location/Qualifiers

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REFERENCE	1 (bases 1 to 11)
AUTHORS	Jurka,J.W.
TITLE	Site directed recombination
JOURNAL	Patent: US 5695977-A 13 09-DEC-1997;
FEATURES	Location/Qualifiers
source	1..11
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ORIGIN	/mol_type="unassigned DNA"
Query Match	30.0%; Score 3; DB 6; Length 11;
Best Local Similarity	100.0%; Pred.No. 0;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RRR 3
Db	 8 RRR 10
RESULT 164	
LOCUS	I84607 11 bp DNA linear PAT 04-APR-1998
DEFINITION	Sequence 13 from patent US 5695977.
ACCESSION	I84607
VERSION	I84607.1 GI:3022127
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 11)
TITLE	Jurka,J.W.
JOURNAL	Site directed recombination
FEATURES	Patent: US 5695977-A 13 09-DEC-1997;
source	Location/Qualifiers
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Query Match	30.0%; Score 3; DB 6; Length 11;
Best Local Similarity	100.0%; Pred.No. 0;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	8 YYY 10
Db	 10 YYY 8
RESULT 165	
LOCUS	AX012240 11 bp DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 2 from Patent WO9955856.
ACCESSION	AX012240
VERSION	AX012240.1 GI:9998301
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
JOURNAL	Nucleic acid enzyme for rna cleavage
FEATURES	Patent: WO 9955856-A 2 04-NOV-1999;
source	ANANVORANICH STRIWART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN PIERRE (CA); UNIV SHERBROOKE (CA)
Location/Qualifiers	1..11
/organism="synthetic construct"	
/mol_type="unassigned DNA"	
/db_xref="taxon:32630"	
/note="synthetic nucleic acid"	
ORIGIN	
Query Match	30.0%; Score 3; DB 6; Length 11;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 1 RRR 3

RESULT 166
AX012240/c
LOCUS AX012240 11 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO955856.
ACCESSION AX012240
VERSION AX012240.1 GI:9998301
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Draper,K.G., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 2 04-NOV-1999;
ANANORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source 1..11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 3 YYY 1

RESULT 167
AX012240/c
LOCUS AX012240 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 445 from Patent EPI288296.
ACCESSION AX012240
VERSION AX012240.1 GI:29787526
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Draper,K.G., McSwiggen,J.A., Holeccek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 445 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1..11
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Nucleic Acid"

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Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WNG 7
Db 3 WNG 5

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 1 RRR 3

RESULT 168
AX012240/c
LOCUS AX012240 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 445 from Patent EPI288296.
ACCESSION AX012240
VERSION AX012240.1 GI:29787526
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Draper,K.G., McSwiggen,J.A., Holeccek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 445 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Location/Qualifiers
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/note="Nucleic Acid"

ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
Db 5 CWV 3

RESULT 169
AX012240/c
LOCUS AX012240 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 446 from Patent EPI288296.
ACCESSION AX012240
VERSION AX012240.1 GI:29787527
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Draper,K.G., McSwiggen,J.A., Holeccek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 446 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/note="Nucleic Acid"

ORIGIN
Query Match 30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
Db 7 CWV 9

RESULT 170
AX012240/c
LOCUS AX012240 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 446 from Patent EPI288296.
ACCESSION AX012240
VERSION AX012240.1 GI:29787527

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/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6
   |||
Db 5 CWW 3

RESULT 175
LOCUS I84596
DEFINITION Sequence 2 from patent US 5695977.
ACCESSION I84596
VERSION I84596.1 GI:3022116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 2 09-DEC-1997;
FEATURES
    source
        location/Qualifiers
            1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 9 YYY 11

RESULT 176
LOCUS I84596/c
DEFINITION Sequence 2 from patent US 5695977.
ACCESSION I84596
VERSION I84596.1 GI:3022116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 2 09-DEC-1997;
FEATURES
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        location/Qualifiers
            1..12
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ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 9 YYY 9

RESULT 177
LOCUS I84596
DEFINITION Sequence 2 from patent US 5695977.
ACCESSION I84596
VERSION I84596.1 GI:3022116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 2 09-DEC-1997;
FEATURES
    source
        location/Qualifiers
            1..12
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ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
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Db 11 RRR 9

RESULT 177
LOCUS I84608
DEFINITION Sequence 14 from patent US 5695977.
ACCESSION I84608
VERSION I84608.1 GI:3022128
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 14 09-DEC-1997;
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ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 9 RRR 11

RESULT 178
LOCUS I84608/c
DEFINITION Sequence 14 from patent US 5695977.
ACCESSION I84608
VERSION I84608.1 GI:3022128
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 14 09-DEC-1997;
FEATURES
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        location/Qualifiers
            1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 11 YYY 9

RESULT 179
LOCUS AX412933
DEFINITION Sequence 697 from Patent WO222675.
ACCESSION AX412933
VERSION AX412933.1 GI:21445391
KEYWORDS
SOURCE Arabidopsis thaliana (chale cresse)
ORGANISM Arabidopsis thaliana
    Arabidopsis thaliana
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
REFERENCE 1
AUTHORS Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
TITLE Plant genes, the expression of which are altered by pathogen
        infection
JOURNAL Patent: WO 0222675-A 697 21-MAR-2002;

```

Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT  
CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,  
Jeffrey L. (US) ; Eulgem, Thomas (US)

# FEATURES

source  
1..12  
Location/Qualifiers  
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## misc\_feature

7..8  
/note="w = adenine or thymine"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
Db 6 CWW 8

RESULT 180  
AX412933/c  
LOCUS AX412933 12 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 697 from Patent WO0222675.  
ACCESSION AX412933  
VERSION AX412933.1 GI:21445391

KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
AUTHORS Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.  
TITLE Plant genes, the expression of which are altered by pathogen infection

JOURNAL  
Patent: WO 0222675-A 697 21-MAR-2002;  
Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT  
CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,  
Jeffrey L. (US) ; Eulgem, Thomas (US)

# FEATURES

source  
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Location/Qualifiers  
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## misc\_feature

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/note="w = adenine or thymine"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7  
Db 8 WWG 6

RESULT 181  
AX412937a  
LOCUS AX412937a 12 bp DNA linear PAT 09-DEC-2003  
DEFINITION Sequence 3 from Patent WO03066867.  
ACCESSION AX412937a  
VERSION AX412937a.1 GI:39646850

KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Andreas,S. and Faust,N.  
TITLE Genetically engineered phic31&minus;integrase genes  
JOURNAL Patent: WO 03066867-A 3 14-AUG-2003;

ARTEMIS Pharmaceuticals GmbH (DE)  
Location/Qualifiers

1..12  
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/note="Description of Artificial Sequence: splice acceptor sequence"

## misc\_feature

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/note="Y is T or C"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

RESULT 182  
AX816374/c  
LOCUS AX816374 12 bp DNA linear PAT 09-DEC-2003  
DEFINITION Sequence 3 from Patent WO03066867.  
ACCESSION AX816374  
VERSION AX816374.1 GI:39646850

KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Andreas,S. and Faust,N.  
TITLE Genetically engineered phic31&minus;integrase genes  
JOURNAL Patent: WO 03066867-A 3 14-AUG-2003;  
ARTEMIS Pharmaceuticals GmbH (DE)

# FEATURES

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Location/Qualifiers  
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## misc\_feature

1..7  
/note="Y is T or C"

## ORIGIN

Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 7 RRR 5

RESULT 183  
AX816375  
LOCUS AX816375 12 bp DNA linear PAT 09-DEC-2003  
DEFINITION Sequence 4 from Patent WO03066867.  
ACCESSION AX816375  
VERSION AX816375.1 GI:39646851

KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Andreas,S. and Faust,N.  
TITLE Genetically engineered phic31&minus;integrase genes  
JOURNAL Patent: WO 03066867-A 4 14-AUG-2003;  
ARTEMIS Pharmaceuticals GmbH (DE)

# FEATURES

source  
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Location/Qualifiers

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misc_feature 1..7
/note="Y is T or C"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 YYY 10
Db 1 YYY 3
RESULT 184
AX816375/c
LOCUS
DEFINITION AX816375 12 bp DNA linear PAT 09-DEC-2003
ACCESSION AX816375
VERSION AX816375.1 GI:39646851
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1
AUTHORS Andreas,S. and Faust,N.
TITLE Genetically engineered phic31minus;integrase genes
JOURNAL Patent: WO 0306867-A 4 14-AUG-2003;
ARTEMIS Pharmaceuticals GmbH (DE)
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/note="Description of Artificial Sequence: splice acceptor site"
misc_feature 1..7
/note="Y is T or C"
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Query Match 30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 7 RRR 5
RESULT 185
BD074027
LOCUS
DEFINITION BD074027 12 bp DNA linear PAT 27-AUG-2002
Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter.
ACCESSION BD074027
VERSION BD074027.1 GI:22619630
KEYWORDS JP 2001512679-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Albert,B.P., Mels,J.R., Lee,W.O. and Nei,B.A.
TITLE Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter
JOURNAL Patent: JP 2001512679-A 9 28-AUG-2001;
COMMENT OS Unidentified

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PN JP 2001512679-A/9
PD 28-AUG-2001
PF 23-JUL-1998 JP 2000506328
PR 03-AUG-1997 US 60/054812,14-APR-1998 US 60/081751 PI
BECKER PRESTON ALBERT,JOHNSON RADOLF MELS,WALTER OM LEE,BERITY
PI ADRIAN NEIL
PC C12N15/09,A61K45/00,A61P25/28,C12N5/10,C12Q1/68,G01N33/15, PC
G01N33/50,
PC C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Human glial cell-line derived neurotrophic factor promoter, vector
CC containing the promoter, and method for screening a compound by the
CC promoter
CC FH key Location/Qualifiers
CC FT source 1..12
FT /organism='Unidentified'.
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/db_xref="taxon:32644"
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Db 1 YYY 3
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LOCUS
DEFINITION BD074027 12 bp DNA linear PAT 27-AUG-2002
Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter.
ACCESSION BD074027
VERSION BD074027.1 GI:22619630
KEYWORDS JP 2001512679-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Albert,B.P., Mels,J.R., Lee,W.O. and Nei,B.A.
TITLE Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter
JOURNAL Patent: JP 2001512679-A 9 28-AUG-2001;
COMMENT OS Unidentified
F HOFFMANN LA ROCHE AG
PN JP 2001512679-A/9
PD 28-AUG-2001
PF 23-JUL-1998 JP 2000506328
PR 03-AUG-1997 US 60/054812,14-APR-1998 US 60/081751 PI
BECKER PRESTON ALBERT,JOHNSON RADOLF MELS,WALTER OM LEE,BERITY
PI ADRIAN NEIL
PC C12N15/09,A61K45/00,A61P25/28,C12N5/10,C12Q1/68,G01N33/15, PC
G01N33/50,
PC C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Human glial cell-line derived neurotrophic factor promoter, vector
CC containing the promoter, and method for screening a compound by the
CC promoter
CC FH key Location/Qualifiers
CC FT source 1..12

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RESULT 187
LOCUS      I27012      13 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 33 from patent US 5563036.
ACCESSION I27012
VERSION I27012.1 GI:1817788
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 33 08-OCT-1996;
FEATURES Location/Qualifiers
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RESULT 188
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VERSION I27012.1 GI:1817788
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 33 08-OCT-1996;
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RESULT 189
LOCUS      I84597      13 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 3 from patent US 5695977.
ACCESSION I84597
VERSION I84597.1 GI:3022117
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 3 09-DEC-1997;
FEATURES Location/Qualifiers
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ACCESSION I84597
VERSION I84597.1 GI:3022117
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
JOURNAL Patent: US 5695977-A 3 09-DEC-1997;
FEATURES Location/Qualifiers
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LOCUS      I84609      13 bp      DNA      linear      PAT 04-APR-1998
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ACCESSION I84609
VERSION I84609.1 GI:3022129
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Jurka,J.W.
TITLE Site directed recombination
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I84609/c
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DEFINITION Sequence 15 from patent US 5695977.
ACCESSION I84609
VERSION I84609.1 GI:3022129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Jurka,J.W.
  TITLE Site directed recombination
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RESULT 193
AX235305
LOCUS AX235305 13 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 7 from Patent WO0162967.
ACCESSION AX235305
VERSION AX235305.1 GI:15593850
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Vidar,B.Z. and Katzir,N.
  TITLE A method that compares genomic sequences
  JOURNAL Patent: WO 0162967-A 7 30-AUG-2001;
  Genena Ltd. (IL) ; Agricultural Research Organization Neve Ya'Ar
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RESULT 195
AR134892
LOCUS AR134892 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6194211.
ACCESSION AR134892
VERSION AR134892.1 GI:14123797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Richards,C.Ann. and Huber,B.
  TITLE transcriptional regulatory sequence of carcinoembryonic antigen for
  expression targeting
  JOURNAL Patent: US 6194211-A 8 27-FEB-2001;
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RESULT 196
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LOCUS AR134892 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6194211.
ACCESSION AR134892

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VERSION      ARI34892.1  GI:14123797
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 14)
AUTHORS     Richards,C.Ann. and Huber,B.
TITLE       Transcriptional regulatory sequence of carcinoembryonic antigen for
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JOURNAL     Patent: US 6194211-A 8 27-FEB-2001;
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ACCESSION  ARI38914
VERSION    ARI38914.1  GI:14481259
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE     Genomic sequences for protein production and delivery
JOURNAL   Patent: US 6200778-A 7 13-MAR-2001;
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Query Match      30.0%; Score 3; DB 6; Length 14;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 198
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ACCESSION  ARI38914
VERSION    ARI38914.1  GI:14481259
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE     Genomic sequences for protein production and delivery
JOURNAL   Patent: US 6200778-A 7 13-MAR-2001;
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DEFINITION Sequence 8 from patent US 6242218.
ACCESSION  ARI56467
VERSION    ARI56467.1  GI:15125171
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE     Genomic sequences for protein production and delivery
JOURNAL   Patent: US 6242218-A 8 05-JUN-2001;
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DEFINITION Sequence 8 from patent US 6242218.
ACCESSION  ARI56467
VERSION    ARI56467.1  GI:15125171
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
TITLE     Genomic sequences for protein production and delivery
JOURNAL   Patent: US 6242218-A 8 05-JUN-2001;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 15:16:19 ; Search time 386 Seconds  
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135.995 Million cell updates/sec

Title: US-09-813-824A-3

Perfect score: 10

Sequence: 1 RRRCCWGGYY 10

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Searched: 4134886 seqs, 2624710521 residues

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11: Geneseq2003ds.\*

12: Geneseq2004s.\*

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#### SUMMARIES

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10	10	100.0	10 4	AAQ31886 p53 bindi
11	10	100.0	10 9	ACA62195 Consensus
12	10	100.0	10 9	ACA62195 Consensus
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692	3	30.0	26	3	AAZ93043	Aaz93043 High-affi	765	3	30.0	27	3	AAZ99852	Aaz99852 PCR prime
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704	3	30.0	26	6	ABK67434	Abk67434 Calcium t	777	3	30.0	27	4	AAZ99865	Aaz99865 Degenerat
705	3	30.0	26	6	ABK67434	Abk67434 Calcium t	C 778	3	30.0	27	6	ABK61413	Abk61413 SELEX pro
706	3	30.0	26	10	ADC16267	Adc16267 Chlamydia	779	3	30.0	27	6	ABK61413	Abk61413 SELEX pro
707	3	30.0	26	10	ADC16267	Adc16267 Chlamydia	C 780	3	30.0	27	6	ABK61413	Abk61413 SELEX pro
708	3	30.0	26	10	ADP67807	Adf67807 SELEX-rel	781	3	30.0	27	6	ABV74339	Abv74339 Ribozyme
709	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 782	3	30.0	27	8	ACC47722	Acc47722 A. niger
710	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	783	3	30.0	27	9	ACD13457	Accl13457 Degenerat
711	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 784	3	30.0	27	9	ACD13457	Accl13457 Degenerat
712	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	785	3	30.0	27	9	ACD13457	Accl13457 Degenerat
713	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 786	3	30.0	27	9	ACD13457	Accl13457 Degenerat
714	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	787	3	30.0	27	9	ACD13457	Accl13457 Degenerat
715	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 788	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
716	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	789	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
717	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 790	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
718	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	791	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
719	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 792	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
720	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	793	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
721	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 794	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
722	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	795	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
723	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 796	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
724	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	797	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
725	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 798	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
726	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	799	3	30.0	27	10	ADG39355	Adg39355 SELEX ass
727	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 800	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
728	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	801	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
729	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 802	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
730	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	803	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
731	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 804	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
732	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	805	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
733	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 806	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
734	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	807	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
735	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 808	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
736	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	809	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
737	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 810	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
738	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	811	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
739	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 812	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
740	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	813	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
741	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 814	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
742	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	815	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
743	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 816	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
744	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	817	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
745	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 818	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
746	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	819	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
747	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 820	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
748	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	821	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
749	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 822	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
750	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	823	3	30.0	27	12	ADG39355	Adg39355 SELEX ass
751	3	30.0	26	12	ADG39355	Adg39355 SELEX ass	C 824	3	30.0	27	12	ADG39355	Adg39355 SELEX ass





971 3 30.0 31 12 ADN97028 Immunosti  
 c 972 3 30.0 31 12 ADN97028  
 c 973 3 30.0 32 2 Aaq06407 Probe for  
 c 974 3 30.0 32 2 Aaq06407  
 c 975 3 30.0 32 2 AAX58849 Hyaluron  
 c 976 3 30.0 32 2 AAX58849  
 c 977 3 30.0 32 2 AAX58849  
 c 978 3 30.0 32 2 AAX21259  
 c 979 3 30.0 32 2 AAX21259 Primer PR  
 c 980 3 30.0 32 3 AAA98231 Human ret  
 c 981 3 30.0 32 3 AAA98231  
 c 982 3 30.0 32 8 ABQ77386 Parsley F  
 c 983 3 30.0 32 8 ABQ77386  
 c 984 3 30.0 32 8 ABV74015 Isoflavon  
 c 985 3 30.0 32 8 ABV74015  
 c 986 3 30.0 32 10 ADF61701  
 c 987 3 30.0 32 10 ADF61701  
 c 988 3 30.0 32 12 ADN97019 Immunosti  
 c 989 3 30.0 32 12 ADN97019  
 c 990 3 30.0 32 12 ADN96964  
 c 991 3 30.0 32 12 ADN96964  
 c 992 3 30.0 32 12 ADN97039 Immunosti  
 c 993 3 30.0 32 12 ADN97039  
 c 994 3 30.0 32 12 ADN97029 Immunosti  
 c 995 3 30.0 32 12 ADN97029  
 c 996 3 30.0 33 2 Aaq31144 Probe 113  
 c 997 3 30.0 33 2 Aaq31144  
 c 998 3 30.0 33 2 Aaq31131 Probe 100  
 c 999 3 30.0 33 2 Aaq31131  
 c1000 3 30.0 33 2 Aaq31134 Probe 103  
 Aaq31134 Probe 103

## ALIGNMENTS

RESULT 1  
 Aaq31948  
 ID Aaq31948 standard; DNA; 10 BP.  
 AC Aaq31948;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-APR-1993 (first entry)  
 XX  
 XX Monomeric p53-specific DNA binding site.  
 XX  
 XX P53; DNA-binding; cancer; neoplasia; tumour; ds.  
 XX  
 XX Synthetic.  
 XX  
 XX EP518650-A2.  
 XX  
 XX 16-DEC-1992.  
 XX  
 XX 10-JUN-1992; 92EP-00305333.  
 XX  
 XX 14-JUN-1991; 91US-00715182.  
 PR 31-MAR-1992; 92US-00860758.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 XX Vogelstein B, Kinzler KW, Sherman MI;  
 XX WPI; 1992-417505/51.  
 XX  
 XX  
 XX Detection and expression of wild type p53 protein - useful for diagnosing  
 PT and treating cancers, and for screening potential chemotherapeutic  
 PT agents.  
 XX  
 XX Claim 22; Page 24; 51pp; English.  
 PS  
 XX Wild-type p53 protein binds specific fragments of human chromosomal DNA.

CC Each fragment contains no more than one monomer of the double stranded  
 CC sequence shown separated by 0-13 base pairs. Some of these sequences are  
 CC found near the origin of replication of certain animal viruses and animal  
 CC cells. Four mutant forms of p53 protein which are commonly found in human  
 CC tumours do not have the ability to bind to these sequences. Thus a  
 CC function of p53 may be mediated by its ability to bind specific DNA  
 CC sequences in the human genome. The sequence shown is a consensus sequence  
 CC for p53 DNA binding. When inserted upstream and adjacent to a reporter  
 CC gene the sequence allows identification of wild type p53, and such a  
 CC construct could be used for diagnosis of p53 mutations and onset and  
 CC development of various cancers. The construct may also be used to screen  
 CC potential chemotherapeutic agents and to identify agents which  
 CC specifically bind p53-specific DNA. Also wild-type p53 gene function may  
 CC be restored to neoplastic cells having a mutation in their p53 gene. See  
 CC also Aaq31949-84. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;  
 Query Match 100.0%; Score 10; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCRCWGGYY 10  
 Db 1 RRCRCWGGYY 10  
 |||||  
 |||||  
 RESULT 2  
 Aaq31948/c  
 ID Aaq31948 standard; DNA; 10 BP.  
 XX  
 AC Aaq31948;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-APR-1993 (first entry)  
 XX  
 XX Monomeric p53-specific DNA binding site.  
 DE  
 XX P53; DNA-binding; cancer; neoplasia; tumour; ds.  
 XX  
 XX Synthetic.  
 OS  
 XX EP518650-A2.  
 PN  
 XX 16-DEC-1992.  
 PD  
 XX 10-JUN-1992; 92EP-00305333.  
 PF  
 XX 14-JUN-1991; 91US-00715182.  
 PR 31-MAR-1992; 92US-00860758.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 XX Vogelstein B, Kinzler KW, Sherman MI;  
 PI WPI; 1992-417505/51.  
 XX  
 XX  
 XX Detection and expression of wild type p53 protein - useful for diagnosing  
 PT and treating cancers, and for screening potential chemotherapeutic  
 PT agents.  
 XX  
 XX Claim 22; Page 24; 51pp; English.  
 PS  
 XX Wild-type p53 protein binds specific fragments of human chromosomal DNA.  
 CC Each fragment contains no more than one monomer of the double stranded  
 CC sequence shown separated by 0-13 base pairs. Some of these sequences are  
 CC found near the origin of replication of certain animal viruses and animal  
 CC cells. Four mutant forms of p53 protein which are commonly found in human  
 CC tumours do not have the ability to bind to these sequences. Thus a  
 CC function of p53 may be mediated by its ability to bind specific DNA  
 CC sequences in the human genome. The sequence shown is a consensus sequence  
 CC for p53 DNA binding. When inserted upstream and adjacent to a reporter

CC gene the sequence allows identification of wild type p53, and such a  
 CC construct could be used for diagnosis of p53 mutations and onset and  
 CC development of various cancers. The construct may also be used to screen  
 CC potential chemotherapeutic agents and to identify agents which  
 CC specifically bind p53-specific DNA. Also wild-type p53 gene function may  
 CC be restored to neoplastic cells having a mutation in their p53 gene. See  
 CC also AAQ31949-84. (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

# RESULT 3

AAV45242  
 ID AAV45242 standard; DNA; 10 BP.

XX AC AAV45242;

XX DT 09-NOV-1998 (first entry)

XX DE Human nerve growth factor exon promoter consensus binding motif.

XX KW NGF; nerve growth factor; treatment; promoter; neurodegenerative disease;  
 consensus binding motif; ds.

XX OS Homo sapiens.

XX PN WO9835027-A2.

XX PD 13-AUG-1998.

XX PF 12-JAN-1998; 98WO-US000396.

XX PR 06-FEB-1997; 97US-0038212P.

XX PA (HMRI ) HOECHST MARION ROUSSEL INC.

XX PI Linnik MD, Racke MM, Krakowsky JM, Subramaniam A;

XX DR WPI; 1998-447224/38.

XX PT Compounds increasing transcription of endogenous human nerve growth  
 factor - using vector containing the growth factor, for treating e.g.  
 neurodegenerative diseases.

XX PS Example 8; Page 49; 89pp; English.

XX CC The sequence is that of a consensus binding motif found in human nerve  
 CC growth factor (NGF) promoter regions. These can be used to screen for and  
 CC characterise compounds able to modulate transcription from the hNGF  
 CC promoters. Such compounds are useful in the treatment of e.g.  
 CC neurodegenerative diseases. The compounds which modulate transcriptional  
 CC activity of endogenous NGF promoters, especially in the brain, can more  
 CC easily pass through the blood-brain barrier than exogenously administered  
 CC NGF or fragments

XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
 |||||  
 Db 1 RRRCWGYYY 10

# RESULT 4

AAV45242/c

ID AAV45242 standard; DNA; 10 BP.

XX AC AAV45242;

XX DT 09-NOV-1998 (first entry)

XX DE Human nerve growth factor exon promoter consensus binding motif.

XX KW NGF; nerve growth factor; treatment; promoter; neurodegenerative disease;  
 consensus binding motif; ds.

XX OS Homo sapiens.

XX PN WO9835027-A2.

XX PD 13-AUG-1998.

XX PF 12-JAN-1998; 98WO-US000396.

XX PR 06-FEB-1997; 97US-0038212P.

XX PA (HMRI ) HOECHST MARION ROUSSEL INC.

XX PI Linnik MD, Racke MM, Krakowsky JM, Subramaniam A;

XX DR WPI; 1998-447224/38.

XX PT Compounds increasing transcription of endogenous human nerve growth  
 factor - using vector containing the growth factor, for treating e.g.  
 neurodegenerative diseases.

XX PS Example 8; Page 49; 89pp; English.

XX CC The sequence is that of a consensus binding motif found in human nerve  
 CC growth factor (NGF) promoter regions. These can be used to screen for and  
 CC characterise compounds able to modulate transcription from the hNGF  
 CC promoters. Such compounds are useful in the treatment of e.g.  
 CC neurodegenerative diseases. The compounds which modulate transcriptional  
 CC activity of endogenous NGF promoters, especially in the brain, can more  
 CC easily pass through the blood-brain barrier than exogenously administered  
 CC NGF or fragments

XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

# RESULT 5

AAV25510

ID AAV25510 standard; DNA; 10 BP.

XX AC AAV25510;

XX DT 09-JUL-1998 (first entry)

XX DE p53 binding site motif.

XX KW Human; bax promoter; apoptosis; autoimmune disease; cancer;

XX KW Alzheimer's disease; Parkinson's disease; stroke; p53 binding site motif;  
 ds.

XX OS Homo sapiens.

XX PN US744310-A.

```

XX PD 28-APR-1998.
XX PF 29-JUL-1996; 96US-00688145.
XX PR 29-JUL-1996; 96US-00688145.
XX PA (BURN-) BURNHAM INST.
XX PI Reed JC;
XX DR WPI; 1998-271064/24.
XX PT New box gene promoter sequence(s) - are useful for identifying agents
XX PT that regulate bax gene expression, e.g. to regulate apoptosis in tumour
XX PT cells.
XX PS Example II; Col 31-32; 29pp; English.
XX CC The present p53 binding site motif can be found in the human bax
XX CC promoter, i.e. nucleotides -3885 to -1 of the bax gene. Bax expression in
XX CC a cell plays a central role in apoptosis. The control elements of the DNA
XX CC encoding this protein are poorly understood. In certain autoimmune
XX CC diseases, e.g. Alzheimer's or Parkinson's disease or strokes, a high
XX CC level of cell death occurs and conversely in certain cancers, apoptosis
XX CC is reduced. The promoter and its related molecules are useful for
XX CC researching the rest of the controlling elements, and in assays for
XX CC screening agents that can regulate bax activity
XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWGYYY 10
Db |||||
1 RRCWGWGYYY 1

RESULT 6
AAV25510/c
ID AAV25510 standard; DNA; 10 BP.
AC AAV25510;
XX 09-JUL-1998 (first entry)
DT p53 binding site motif.
DE Human; bax promoter; apoptosis; autoimmune disease; cancer;
KW Alzheimer's disease; Parkinson's disease; stroke; p53 binding site motif;
KW ds.
XX Homo sapiens.
XX US5744310-A.
XX 28-APR-1998.
XX 29-JUL-1996; 96US-00688145.
XX PR 29-JUL-1996; 96US-00688145.
XX PA (BURN-) BURNHAM INST.
XX PI Reed JC;
XX DR WPI; 1998-271064/24.
XX PT New box gene promoter sequence(s) - are useful for identifying agents
XX PT that regulate bax gene expression, e.g. to regulate apoptosis in tumour
XX PT cells.

```

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XX PS Example II; Col 31-32; 29pp; English.
XX CC The present p53 binding site motif can be found in the human bax
XX CC promoter, i.e. nucleotides -3885 to -1 of the bax gene. Bax expression in
XX CC a cell plays a central role in apoptosis. The control elements of the DNA
XX CC encoding this protein are poorly understood. In certain autoimmune
XX CC diseases, e.g. Alzheimer's or Parkinson's disease or strokes, a high
XX CC level of cell death occurs and conversely in certain cancers, apoptosis
XX CC is reduced. The promoter and its related molecules are useful for
XX CC researching the rest of the controlling elements, and in assays for
XX CC screening agents that can regulate bax activity
XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWGYYY 10
Db |||||
1 RRCWGWGYYY 1

RESULT 7
AAF31886
ID AAF31886 standard; DNA; 10 BP.
AC AAF31886;
XX 12-APR-2001 (first entry)
DT p53 binding site consensus sequence.
DE KARP-1; Ku86 autoantigen related protein; cancer; p53 binding site;
KW immune deficiency disorder; biliary tract cancer; leucine zipper protein;
KW cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
XX Homo sapiens.
XX OS US6171857-B1.
XX PN 09-JAN-2001.
XX PD 16-OCT-1998; 98US-00173914.
XX PF 17-OCT-1997; 97US-0064557P.
XX PR (UYBR-) UNIV BROWN RES FOUND.
XX PA Hendrickson EA;
XX PI WPI; 2001-146208/15.
XX DR Novel nucleic acids encoding leucine zipper protein, KARP-1 polypeptide,
XX PT useful for treating cancer and immune deficiency disorder.
XX PS Example 10; Col 47; 61pp; English.
XX CC The present sequence is given in a specification relating to an isolated
XX CC Ku86 Autoantigen Related Protein (KARP-1) nucleic acid molecule. The KARP
XX CC -1 nucleic acid and KARP-1 protein are useful for the treatment and/or
XX CC diagnosis of diseases such as cancer and immune deficiency disorders.
XX CC They are useful in combination with a KARP-1 inhibitor that inhibits
XX CC double stranded DNA base repair. Inhibitors of KARP-1 are useful in the
XX CC diagnosis or treatment of conditions characterised by the loss of KARP-1
XX CC activity and in the treatment of cancer, e.g. biliary tract cancer
XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

KW seedless fruit; male sterility; proteic killer gene system; ds.
XX Unidentified.
OS
XX WO200105421-A1.
XX
XX PD 25-JAN-2001.
XX
XX PF 17-JUL-2000; 2000WO-GB002743.
XX
XX PR 16-JUL-1999; 99GB-00016810.
XX
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI De La Cueva Mendez G, Laskey RA, Mills AD, Diaz Orejas R;
XX WPI; 2001-182641/18.
XX
XX PT Inhibiting cell proliferation and/or cell cycle progression used for
XX treating tumors, cancer and psoriasis, involves using toxins and
XX toxin/antidote system based on bacterial system.
XX
XX PS Disclosure; Page 27; 64pp; English.
XX
XX CC The present invention describes a method of inhibiting cell proliferation
XX or cell cycle progression, involving providing eukaryotic cells with a
XX bacterial toxin and an antidote to said toxin under appropriate control
XX for selective cell cycle inhibition or killing of target cells. This is
XX useful in the treatment of cancer, arteriosclerosis, psoriasis and other
XX hyperproliferative diseases, in the production of male sterile, seedless
XX and disease resistant plants, and in the production of animal knock-outs
XX which enable the study of organogenesis and developmental control. The
XX present sequence is the p53 binding sequence which is described in the
XX specification
XX
XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;
XX
XX Query Match 100.0%; Score 10; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RRRCWGYYY 10
XX Db 1 RRRCWGYYY 10
XX
XX RESULT 10
XX AAF58009/c
XX ID AAF58009 standard; DNA; 10 BP.
XX
XX AC AAF58009;
XX
XX XX
XX DT 26-APR-2001 (first entry)
XX
XX XX
XX DE Wild-type p53 binding consensus sequence.
XX
XX KW Bacterial toxin; antidote; cell death; apoptosis; developmental control;
XX organogenesis; cancer; psoriasis; arteriosclerosis; knock-out;
XX KW seedless fruit; male sterility; proteic killer gene system; ds.
XX
XX OS Unidentified.
XX
XX XX
XX PN WO200105421-A1.
XX
XX PD 25-JAN-2001.
XX
XX PF 17-JUL-2000; 2000WO-GB002743.
XX
XX PR 16-JUL-1999; 99GB-00016810.
XX
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI De La Cueva Mendez G, Laskey RA, Mills AD, Diaz Orejas R;
XX
XX KW seedless fruit; male sterility; proteic killer gene system; ds.
XX Unidentified.
XX
XX OS
XX PN WO200105421-A1.
XX
XX PD 25-JAN-2001.
XX
XX PF 17-JUL-2000; 2000WO-GB002743.
XX
XX PR 16-JUL-1999; 99GB-00016810.
XX
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI De La Cueva Mendez G, Laskey RA, Mills AD, Diaz Orejas R;

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QY 1 RRRCWGYYY 10
Db 1 RRRCWGYYY 10

RESULT 8
AAF31886/c
ID AAF31886 standard; DNA; 10 BP.
XX
XX AC AAF31886;
XX
XX DT 12-APR-2001 (first entry)
XX
XX DE p53 binding site consensus sequence.
XX
XX KW KARP-1; Ku86 autoantigen related protein; cancer; p53 binding site;
XX immune deficiency disorder; biliary tract cancer; leucine zipper protein;
XX cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
XX
XX OS Homo sapiens.
XX
XX PN US6171857-B1.
XX
XX PD 09-JAN-2001.
XX
XX PF 16-OCT-1998; 98US-00173914.
XX
XX PR 17-OCT-1997; 97US-0064557P.
XX
XX PA (UYBR-) UNIV BROWN RES FOUND.
XX
XX PI Hendrickson EA;
XX
XX DR WPI; 2001-146208/15.
XX
XX PT Novel nucleic acids encoding leucine zipper protein, KARP-1 polypeptide,
XX useful for treating cancer and immune deficiency disorder.
XX
XX PS Example 10; Col 47; 61pp; English.
XX
XX CC The present sequence is given in a specification relating to an isolated
XX Ku86 Autoantigen Related Protein (KARP-1) nucleic acid molecule. The KARP
XX -1 nucleic acid and KARP-1 protein are useful for the treatment and/or
XX diagnosis of diseases such as cancer and immune deficiency disorders.
XX They are useful in combination with a KARP-1 inhibitor that inhibits
XX double stranded DNA base repair. Inhibitors of KARP-1 are useful in the
XX diagnosis or treatment of conditions characterised by the loss of KARP-1
XX activity and in the treatment of cancer, e.g. biliary tract cancer
XX
XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;
XX
XX Query Match 100.0%; Score 10; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RRRCWGYYY 10
XX Db 10 RRRCWGYYY 1
XX
XX RESULT 9
XX AAF58009
XX ID AAF58009 standard; DNA; 10 BP.
XX
XX AC AAF58009;
XX
XX XX
XX DT 26-APR-2001 (first entry)
XX
XX DE Wild-type p53 binding consensus sequence.
XX
XX KW Bacterial toxin; antidote; cell death; apoptosis; developmental control;
XX organogenesis; cancer; psoriasis; arteriosclerosis; knock-out;

```

XX WPI; 2001-182641/18.  
XX  
XX Inhibiting cell proliferation and/or cell cycle progression used for  
PT treating tumors, cancer and psoriasis, involves using toxins and  
PT toxin/antidote system based on bacterial system.  
XX  
XX Disclosure; Page 27; 54pp; English.  
XX  
XX The present invention describes a method of inhibiting cell proliferation  
CC or cell cycle progression, involving providing eukaryotic cells with a  
CC bacterial toxin and an antidote to said toxin under appropriate control  
CC for selective cell cycle inhibition or killing of target cells. This is  
CC useful in the treatment of cancer, arteriosclerosis, psoriasis and other  
CC hyperproliferative diseases, in the production of male sterile, seedless  
CC and disease resistant plants, and in the production of animal knock-outs  
CC which enable the study of organogenesis and developmental control. The  
CC present sequence is the p53 binding sequence which is described in the  
CC specification  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;  
  
Query Match 100.0%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRCWGWGYY 10  
Db 10 RRCWGWGYY 1  
  
RESULT 11  
ACA62195  
ID ACA62195 standard; DNA; 10 BP.  
XX  
XX ACA62195;  
XX  
XX 08-AUG-2003 (first entry)  
XX  
XX Consensus p53 recognition sequence.  
XX  
XX p53; ds; genome instability disease; cancer; DNA binding factor;  
KW proximity-based luminescence detection.  
KW  
XX Synthetic.  
XX  
XX US2003049625-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 13-AUG-2001; 2001US-00928385.  
XX  
XX 13-AUG-2001; 2001US-00928385.  
XX  
XX (UYSL-) UNIV SAINT LOUIS.  
XX  
XX Heyduk T;  
XX  
XX WPI; 2003-456598/43.  
XX  
XX Detecting or quantifying sample DNA binding factors, or determining  
PT activity of DNA binding factor, by detecting binding of DNA binding  
PT factor with DNA binding element by proximity-based luminescence  
PT detection.  
XX  
XX Example 8; Page 15; 43pp; English.  
XX  
XX The invention relates to a method of detecting/quantifying DNA binding  
CC factors in a sample, or determining activity of DNA binding factors,  
CC involves combining two sets of nucleic acid components (NCs) with sample,  
CC where each NC comprises DNA binding element (DE), one NC is labelled with  
CC fluorescence donor and other NC labeled with fluorescence acceptor, to  
CC emit light at unique wavelength and detecting DNA binding factors-DE  
CC

CC binding by proximity-based luminescence detection. The method is useful  
CC for detecting or quantifying DNA binding factors in a sample and for  
CC determining the activity of DNA binding factor. The method is useful for  
CC determining the amount of an analyte in a sample, where the association  
CC of DNA binding factors and DE is mediated by the analyte e.g. secondary  
CC messenger molecule (e.g. cAMP), cellular event, drug agent, reagent,  
CC prospective drug, prospective agent and prospective reagent. The method  
CC is also useful for diagnosing a disease mediated by a DNA binding factor  
CC in a human patient who is suffering from a type of cancer or disease of  
CC genome instability. The methods are useful for detecting mediating  
CC analytes, to diagnose diseases, and/or to screen for drugs that mediate  
CC the activity of DNA binding factors. The method is inexpensive, simple  
CC and is compatible with high-throughput detection formats. The present  
CC sequence represents the consensus p53 recognition sequence  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;  
  
Query Match 100.0%; Score 10; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRCWGWGYY 10  
Db 1 RRCWGWGYY 10  
  
RESULT 12  
ACA62195/c  
ID ACA62195 standard; DNA; 10 BP.  
XX  
XX ACA62195;  
XX  
XX 08-AUG-2003 (first entry)  
XX  
XX Consensus p53 recognition sequence.  
XX  
XX p53; ds; genome instability disease; cancer; DNA binding factor;  
KW proximity-based luminescence detection.  
KW  
XX Synthetic.  
XX  
XX US2003049625-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 13-AUG-2001; 2001US-00928385.  
XX  
XX 13-AUG-2001; 2001US-00928385.  
XX  
XX (UYSL-) UNIV SAINT LOUIS.  
XX  
XX Heyduk T;  
XX  
XX WPI; 2003-456598/43.  
XX  
XX Detecting or quantifying sample DNA binding factors, or determining  
PT activity of DNA binding factor, by detecting binding of DNA binding  
PT factor with DNA binding element by proximity-based luminescence  
PT detection.  
XX  
XX Example 8; Page 15; 43pp; English.  
XX  
XX The invention relates to a method of detecting/quantifying DNA binding  
CC factors in a sample, or determining activity of DNA binding factors,  
CC involves combining two sets of nucleic acid components (NCs) with sample,  
CC where each NC comprises DNA binding element (DE), one NC is labelled with  
CC fluorescence donor and other NC labeled with fluorescence acceptor, to  
CC emit light at unique wavelength and detecting DNA binding factors-DE  
CC binding by proximity-based luminescence detection. The method is useful  
CC for detecting or quantifying DNA binding factors in a sample and for  
CC determining the activity of DNA binding factor. The method is useful for  
CC determining the amount of an analyte in a sample, where the association  
CC of DNA binding factors and DE is mediated by the analyte e.g. secondary

CC messenger molecule (e.g. cAMP), cellular event, drug agent, reagent,  
 CC prospective drug, prospective agent and prospective reagent. The method  
 CC is also useful for diagnosing a disease mediated by a DNA binding factor  
 CC in a human patient who is suffering from a type of cancer or disease of  
 CC genome instability. The methods are useful for detecting mediating  
 CC analytes, to diagnose diseases, and/or to screen for drugs that mediate  
 CC the activity of DNA binding factors. The method is inexpensive, simple  
 CC and is compatible with high-throughput detection formats. The present  
 CC sequence represents the consensus p53 recognition sequence

SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10  
 |||||  
 Db 10 RRCRCWGGYY 1

RESULT 13  
 ABK91337  
 ID ABK91337 standard; DNA; 19 BP.

XX AC ABK91337;  
 XX 15-NOV-2002 (first entry)  
 XX Human JFY1, p53-binding site, CBS.

XX Human; JFY1; apoptosis; cancer; cellular proliferation; p53;  
 KW gene therapy; neoplastic cancer cell; ds.

OS Homo sapiens.  
 OS Synthetic.

PN WO200264790-A2.

PD 22-AUG-2002.

PF 12-DEC-2001; 2001WO-US047455.

PR 19-DEC-2000; 2000US-0256328P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Yu J, Kinzler KW, Vogelstein B;

XX WPI; 2002-643485/69.

XX New JFY1 proteins and nucleic acids, useful for inducing rapid apoptosis  
 PT in cancer cells, for treating cancers or other diseases characterized by  
 PT unwanted cellular proliferation, and as a substitute for p53 in cancer  
 PT gene therapy.

XX Disclosure; Fig 3; 45pp; English.

CC The invention relates to an isolated and purified JFY1 coding sequence  
 CC and purified JFY1 protein. The JFY1 polynucleotide is useful for inducing  
 CC rapid apoptosis in cancer cells, for treating cancers or other diseases  
 CC characterised by unwanted cellular proliferation, and as a substitute for  
 CC p53 in cancer gene therapy. The expression product of JFY1 may be used as  
 CC an indicator for neoplastic cancer cells and in determining the prognosis  
 CC of a cancer patient. The present sequence represents a human JFY1, p53-  
 CC binding site

SQ Sequence 19 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 15 Other;

Query Match 100.0%; Score 10; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10  
 |||||  
 Db 10 RRCRCWGGYY 19

RESULT 14

ABK91337/c  
 ID ABK91337 standard; DNA; 19 BP.

XX AC ABK91337;

XX 15-NOV-2002 (first entry)

XX Human JFY1, p53-binding site, CBS.

XX Human; JFY1; apoptosis; cancer; cellular proliferation; p53;  
 KW gene therapy; neoplastic cancer cell; ds.

XX Homo sapiens.

OS Synthetic.

PN WO200264790-A2.

PD 22-AUG-2002.

PF 12-DEC-2001; 2001WO-US047455.

PR 19-DEC-2000; 2000US-0256328P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Yu J, Kinzler KW, Vogelstein B;

XX WPI; 2002-643485/69.

XX New JFY1 proteins and nucleic acids, useful for inducing rapid apoptosis  
 PT in cancer cells, for treating cancers or other diseases characterized by  
 PT unwanted cellular proliferation, and as a substitute for p53 in cancer  
 PT gene therapy.

XX Disclosure; Fig 3; 45pp; English.

CC The invention relates to an isolated and purified JFY1 coding sequence  
 CC and purified JFY1 protein. The JFY1 polynucleotide is useful for inducing  
 CC rapid apoptosis in cancer cells, for treating cancers or other diseases  
 CC characterised by unwanted cellular proliferation, and as a substitute for  
 CC p53 in cancer gene therapy. The expression product of JFY1 may be used as  
 CC an indicator for neoplastic cancer cells and in determining the prognosis  
 CC of a cancer patient. The present sequence represents a human JFY1, p53-  
 CC binding site

SQ Sequence 19 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 15 Other;

Query Match 100.0%; Score 10; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCRCWGGYY 10  
 |||||  
 Db 19 RRCRCWGGYY 10

RESULT 15

AAZ51676  
 ID AAZ51676 standard; DNA; 20 BP.

XX AC AAZ51676;

XX 21-JUN-2000 (first entry)

XX Human p53-responsive element consensus sequence.

XX PRG; p53 target; human; p53-responsive element; cell proliferation;

KW consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;  
 KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;  
 KW cell cycle arrest; modulate; treatment; knockout animal;  
 KW cancer susceptibility; ds.  
 XX OS Homo sapiens.  
 XX OS WO200012526-A1.  
 PN 09-MAR-2000.  
 XX 27-AUG-1999; 99WO-US019551.  
 XX 28-AUG-1998; 98US-0098251P.  
 XX (UYPR-) UNIV PRINCETON.  
 PA Horikoshi N, Shenk T;  
 XX WPI; 2000-246724/21.  
 XX New p53-inducible isolated nucleic acid molecule including open reading  
 PT frame encoding human homolog of Drosophila melanogaster peroxidasin,  
 PT useful e.g. in detection and treatment of cancer.  
 XX Example 2; Page 78; 83pp; English.  
 PS The present sequence is the p53-responsive element consensus sequence,  
 CC located on PRG target molecules, that are modulated on induction by p53  
 CC activity. The tumour suppressor gene p53, functions as a transcription  
 CC factor and interacts with this responsive element and activates  
 CC transcription from the promoter. PRG sequences are potential targets of  
 CC p53 regulatory activity and are useful for modulation of cellular  
 CC proliferation. It has cytostatic and immunomodulatory activity. PRG  
 CC polynucleotides, proteins and antibodies are useful as diagnostic and  
 CC therapeutic agents for detection and treatment of cancer and other  
 CC proliferative diseases. The gene/cDNA may be used for gene therapy, to  
 CC restore a gene function downstream of p53, that cannot be activated in  
 CC the p53-deficient tumour cell. Antibodies can be used as inducers of cell  
 CC cycle arrest and/or apoptosis. The DNA sequences can be used to generate  
 CC 'knockout' animals as a model of cancer susceptibility  
 XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 Query Match 100.0%; Score 10; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCWGWGYYY 10  
 Db |||||  
 1 RRCWGWGYYY 10  
 RESULT 16  
 AAZ51676/C  
 ID AAZ51676 standard; DNA; 20 BP.  
 AC AAZ51676;  
 XX 21-JUN-2000 (first entry)  
 DT Human p53-responsive element consensus sequence.  
 DE PRG; p53 target; human; p53-responsive element; cell proliferation;  
 XX consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;  
 KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;  
 KW cell cycle arrest; modulate; treatment; knockout animal;  
 KW cancer susceptibility; ds.  
 XX OS Homo sapiens.  
 XX OS WO200012526-A1.  
 PN 09-MAR-2000.  
 XX 27-AUG-1999; 99WO-US019551.  
 XX 28-AUG-1998; 98US-0098251P.  
 XX (UYPR-) UNIV PRINCETON.  
 PA Horikoshi N, Shenk T;  
 XX WPI; 2000-246724/21.  
 XX New p53-inducible isolated nucleic acid molecule including open reading  
 PT frame encoding human homolog of Drosophila melanogaster peroxidasin,  
 PT useful e.g. in detection and treatment of cancer.  
 XX Example 2; Page 78; 83pp; English.  
 PS The present sequence is the p53-responsive element consensus sequence,  
 CC located on PRG target molecules, that are modulated on induction by p53  
 CC activity. The tumour suppressor gene p53, functions as a transcription  
 CC factor and interacts with this responsive element and activates  
 CC transcription from the promoter. PRG sequences are potential targets of  
 CC p53 regulatory activity and are useful for modulation of cellular  
 CC proliferation. It has cytostatic and immunomodulatory activity. PRG  
 CC polynucleotides, proteins and antibodies are useful as diagnostic and  
 CC therapeutic agents for detection and treatment of cancer and other  
 CC proliferative diseases. The gene/cDNA may be used for gene therapy, to  
 CC restore a gene function downstream of p53, that cannot be activated in  
 CC the p53-deficient tumour cell. Antibodies can be used as inducers of cell  
 CC cycle arrest and/or apoptosis. The DNA sequences can be used to generate  
 CC 'knockout' animals as a model of cancer susceptibility  
 XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 Query Match 100.0%; Score 10; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCWGWGYYY 10  
 Db |||||  
 1 RRCWGWGYYY 10  
 RESULT 17  
 AAL42021  
 ID AAL42021 standard; DNA; 20 BP.  
 AC AAL42021;  
 XX 16-MAY-2002 (first entry)  
 DT Human generic p53 DNA binding site consensus sequence.  
 DE Human; generic p53 DNA binding site consensus sequence; ss;  
 KW chromosomal immunoprecipitation; Chip; target gene discovery;  
 KW coding sequence discovery; regulatory element discovery;  
 KW transcription factor discovery; screening; highly automatable;  
 KW high-throughput analysis.  
 XX OS Homo sapiens.  
 XX OS WO200214550-A2.  
 PN 21-FEB-2002.  
 XX 08-AUG-2001; 2001WO-US024823.  
 XX 14-AUG-2000; 2000US-0225225P.  
 PR (TRAN-) TRANSGENETICS INC.  
 PA Burgess RM, Lunyak V, Noskin L;  
 XX

PD 09-MAR-2000.  
 XX 27-AUG-1999; 99WO-US019551.  
 XX 28-AUG-1998; 98US-0098251P.  
 XX (UYPR-) UNIV PRINCETON.  
 PA Horikoshi N, Shenk T;  
 XX WPI; 2000-246724/21.  
 XX New p53-inducible isolated nucleic acid molecule including open reading  
 PT frame encoding human homolog of Drosophila melanogaster peroxidasin,  
 PT useful e.g. in detection and treatment of cancer.  
 XX Example 2; Page 78; 83pp; English.  
 PS The present sequence is the p53-responsive element consensus sequence,  
 CC located on PRG target molecules, that are modulated on induction by p53  
 CC activity. The tumour suppressor gene p53, functions as a transcription  
 CC factor and interacts with this responsive element and activates  
 CC transcription from the promoter. PRG sequences are potential targets of  
 CC p53 regulatory activity and are useful for modulation of cellular  
 CC proliferation. It has cytostatic and immunomodulatory activity. PRG  
 CC polynucleotides, proteins and antibodies are useful as diagnostic and  
 CC therapeutic agents for detection and treatment of cancer and other  
 CC proliferative diseases. The gene/cDNA may be used for gene therapy, to  
 CC restore a gene function downstream of p53, that cannot be activated in  
 CC the p53-deficient tumour cell. Antibodies can be used as inducers of cell  
 CC cycle arrest and/or apoptosis. The DNA sequences can be used to generate  
 CC 'knockout' animals as a model of cancer susceptibility  
 XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 Query Match 100.0%; Score 10; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCWGWGYYY 10  
 Db |||||  
 20 RRCWGWGYYY 11  
 RESULT 17  
 AAL42021  
 ID AAL42021 standard; DNA; 20 BP.  
 AC AAL42021;  
 XX 16-MAY-2002 (first entry)  
 DT Human generic p53 DNA binding site consensus sequence.  
 DE Human; generic p53 DNA binding site consensus sequence; ss;  
 KW chromosomal immunoprecipitation; Chip; target gene discovery;  
 KW coding sequence discovery; regulatory element discovery;  
 KW transcription factor discovery; screening; highly automatable;  
 KW high-throughput analysis.  
 XX OS Homo sapiens.  
 XX OS WO200214550-A2.  
 PN 21-FEB-2002.  
 XX 08-AUG-2001; 2001WO-US024823.  
 XX 14-AUG-2000; 2000US-0225225P.  
 PR (TRAN-) TRANSGENETICS INC.  
 PA Burgess RM, Lunyak V, Noskin L;  
 XX



XX WPI; 2002-241911/29.  
 XX Utilizing sequential chromosomal immunoprecipitation for discovery and  
 PT characterization of target genes for transcription factors which are of  
 PT DNA binding nature.  
 PS Example; Page 47; 68pp; English.  
 XX The invention comprises a method which utilizes chromosomal  
 CC immunoprecipitation (Chip) procedures for the discovery and  
 CC characterisation of transcription factor target genes. The method of the  
 CC invention is useful for the discovery and characterisation of  
 CC transcription factor target genes. The method is preferably useful for  
 CC the discovery and characterisation of: target genes (e.g. coding  
 CC sequences and regulatory elements); and DNA binding transcription  
 CC factors. The DNA sequences isolated by the method of the invention are  
 CC useful for cross-hybridising against libraries of nucleotide sequences,  
 CC and for screening against arrays of nucleotide sequences. The method of  
 CC the invention is highly automatable, allowing for extensive high-  
 CC throughput analysis of virtually any genetic cascade. The present DNA  
 CC sequence represents a generic p53 DNA binding site consensus sequence  
 XX Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 SQ Query Match 100.0%; Score 10; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRRCWGYYY 10  
 Db 1 RRRCWGYYY 10  
 |||||  
 20 RRRCWGYYY 11

RESULT 18  
 AAL4201/C  
 ID AAL4201 standard; DNA; 20 BP.  
 XX AC AAL4201;  
 XX 16-MAY-2002 (first entry)  
 DE Human generic p53 DNA binding site consensus sequence.  
 XX Human; generic p53 DNA binding site consensus sequence; ss;  
 KW chromosomal immunoprecipitation; Chip; target gene discovery;  
 KW coding sequence discovery; regulatory element discovery;  
 KW transcription factor discovery; screening; highly automatable;  
 KW high-throughput analysis.  
 XX Homo sapiens.  
 OS  
 XX WO200214550-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 08-AUG-2001; 2001WO-US024823.  
 XX 14-AUG-2000; 2000US-0225225P.  
 XX (TRAN-) TRANSGENETICS INC.  
 PA Burgess RM, Lunyak V, Noskin L;  
 PI WPI; 2002-241911/29.  
 XX Utilizing sequential chromosomal immunoprecipitation for discovery and  
 PT characterization of target genes for transcription factors which are of  
 PT DNA binding nature.  
 XX Example; Page 47; 68pp; English.  
 PS The invention comprises a method which utilizes chromosomal  
 CC immunoprecipitation (Chip) procedures for the discovery and  
 CC characterisation of transcription factor target genes. The method of the  
 CC invention is useful for the discovery and characterisation of  
 CC transcription factor target genes. The method is preferably useful for  
 CC the discovery and characterisation of: target genes (e.g. coding  
 CC sequences and regulatory elements); and DNA binding transcription  
 CC factors. The DNA sequences isolated by the method of the invention are  
 CC useful for cross-hybridising against libraries of nucleotide sequences,  
 CC and for screening against arrays of nucleotide sequences. The method of  
 CC the invention is highly automatable, allowing for extensive high-  
 CC throughput analysis of virtually any genetic cascade. The present DNA  
 CC sequence represents a generic p53 DNA binding site consensus sequence  
 XX Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 SQ Query Match 100.0%; Score 10; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRRCWGYYY 10  
 Db 1 RRRCWGYYY 10  
 |||||  
 20 RRRCWGYYY 11

RESULT 19  
 AAD30357  
 ID AAD30357 standard; DNA; 20 BP.  
 XX AC AAD30357;  
 XX 21-MAY-2002 (first entry)  
 DE p53 consensus binding site DNA.  
 XX Testes-specific, vespid and pathogenic protein; RTVP; therapy;  
 KW anti-neoplastic; prostatic neoplasia; prostate carcinoma; cytokine;  
 KW metastatic disease; neoplastic disease; immune system; growth factor;  
 KW cytotatic; ds.  
 XX Unidentified.  
 OS  
 XX WO200206344-A2.  
 PN  
 XX 24-JAN-2002.  
 PD  
 XX 08-JUN-2001; 2001WO-US018487.  
 XX 08-JUN-2000; 2000US-0209989P.  
 XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA Thompson TC, Ren C;  
 PI WPI; 2002-195804/25.  
 DR  
 XX Novel testes-specific, vespid and pathogenic polypeptide useful for  
 PT treating and preventing prostatic neoplastic diseases, such as prostatic  
 PT carcinoma and metastatic carcinoma, has antineoplastic activity.  
 XX Example 1; Page 16; 72pp; English.  
 PS The invention relates to a gene encoding non-human testes-specific,  
 XX vespid and pathogenic protein (RTVP) having anti-neoplastic activity. The  
 CC invention further relates to compositions and methods based on RTVP for  
 CC the treatment, prevention and detection of prostatic neoplasia such as  
 CC prostate carcinoma and associated metastatic disease. Diagnostic kit  
 CC comprising RTVP protein is useful for the detection of neoplastic  
 CC disease. Composition comprising RTVP protein is useful in the diagnosis,  
 CC studying and treatment of prostatic neoplasia such as prostatic carcinoma  
 CC and associated metastatic disease. It is also useful for stimulating  
 CC immune system e.g. cytokines and growth factors in a patient. The present  
 CC sequence is p53 consensus binding site DNA used in the identification of  
 CC mRTVP-1 as a p53 target gene

```
XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;
Query Match 100.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRWGYYY 10
Db 1 RRCRWGYYY 10

RESULT 20
AAD30357/c
ID AAD30357 standard; DNA; 20 BP.
XX AC AAD30357;
XX DT 21-MAY-2002 (first entry)
XX DE p53 consensus binding site DNA.
XX KW Testes-specific, vespid and pathogenic protein; RTVP; therapy;
KW anti-neoplastic; prostatic neoplasia; prostate carcinoma; cytokine;
KW metastatic disease; neoplastic disease; immune system; growth factor;
KW cytostatic; ds.
XX OS Unidentified.
XX PN WO200206344-A2.
XX PD 24-JAN-2002.
XX PF 08-JUN-2001; 2001WO-US018487.
XX PR 08-JUN-2000; 2000US-0209989P.
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX PI Thompson TC, Ren C;
XX DR WPI; 2002-195804/25.
XX PT Novel testes-specific, vespid and pathogenic polypeptide useful for
PT treating and preventing prostatic neoplastic diseases, such as prostatic
PT carcinoma and metastatic carcinoma, has antineoplastic activity.
XX PS Example 1; Page 16; 72pp; English.
XX CC The invention relates to a gene encoding non-human testes-specific,
CC vespid and pathogenic protein (RTVP) having anti-neoplastic activity. The
CC invention further relates to compositions and methods based on RTVP for
CC the treatment, prevention and detection of prostatic neoplasia such as
CC prostate carcinoma and associated metastatic disease. Diagnostic kit
CC comprising RTVP protein is useful for the detection of neoplastic
CC disease. Composition comprising RTVP protein is useful in the diagnosis,
CC studying and treatment of prostatic neoplasia such as prostatic carcinoma
CC and associated metastatic disease. It is also useful for stimulating
CC immune system e.g. cytokines and growth factors in a patient. The present
CC sequence is p53 consensus binding site DNA used in the identification of
CC mRTVP-1 as a p53 target gene
XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;
Query Match 100.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRWGYYY 10
Db 20 RRCRWGYYY 11
```

```
RESULT 21
ADC71586
ID ADC71586 standard; DNA; 20 BP.
XX AC ADC71586;
XX DT 18-DEC-2003 (first entry)
XX DE Degenerate nucleotide Seq ID16 related to apoptosis induction.
XX KW apoptosis; p53; p73; heterooligomer; deltaNp73; cytostatic;
KW p73 transcription; p53 transcription; cancer; neuroblastoma; ss.
XX OS Unidentified.
XX PN WO2003061710-A1.
XX PD 31-JUL-2003.
XX PF 23-JAN-2003; 2003WO-JP000605.
XX PR 25-JAN-2002; 2002JP-00017486.
XX PA (HISM ) HISAMITSU PHARM CO LTD.
XX PA (CHIB-) CHIBA PREFECTURE.
XX PI Nakagawara A;
XX DR WPI; 2003-598710/56.
XX PT Regulators of apoptosis induction by p53 or p73 for treatment and
XX PT prevention of neuroblastoma and other cancers.
XX PS Example 3; SEQ ID NO 16; 65pp; Japanese.
XX CC This invention relates to novel agents which regulate the induction of
XX CC apoptosis by p53 or p73 by formation of a heterooligomer with deltaNp73.
XX CC The invention may have cytostatic activity by acting as an agonist or
XX CC antagonist of p73 and p53 transcription. Agents which regulate the
XX CC induction of apoptosis by p53 or p73 are useful for treatment and
XX CC prevention of cancer, including neuroblastoma. The present sequence is
XX CC that of a degenerate DNA sequence which is related to the invention.
XX SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;
Query Match 100.0%; Score 10; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRWGYYY 10
Db 1 RRCRWGYYY 10

RESULT 22
ADC71586/c
ID ADC71586 standard; DNA; 20 BP.
XX AC ADC71586;
XX DT 18-DEC-2003 (first entry)
XX DE Degenerate nucleotide Seq ID16 related to apoptosis induction.
XX KW apoptosis; p53; p73; heterooligomer; deltaNp73; cytostatic;
KW p73 transcription; p53 transcription; cancer; neuroblastoma; ss.
XX OS Unidentified.
XX PN WO2003061710-A1.
XX PD 31-JUL-2003.
XX
```

PF 23-JAN-2003; 2003WO-JP000605.  
 XX  
 PR 25-JAN-2002; 2002JP-00017486.  
 XX  
 XX (HISM ) HISAMITSU PHARM CO LTD.  
 PA (CHIB-) CHIBA PREFECTURE.  
 XX  
 XX Nakagawara A;  
 XX WPI; 2003-598710/56.  
 DR  
 XX Regulators of apoptosis induction by p53 or p73 for treatment and  
 PT prevention of neuroblastoma and other cancers.  
 XX  
 XX Example 3; SEQ ID NO 16; 65pp; Japanese.  
 XX  
 CC This invention relates to novel agents which regulate the induction of  
 CC apoptosis by p53 or p73 by formation of a heterooligomer with deltaNp73.  
 CC The invention may have cytostatic activity by acting as an agonist or  
 CC antagonist of p73 and p53 transcription. Agents which regulate the  
 CC induction of apoptosis by p53 or p73 are useful for treatment and  
 CC prevention of cancer, including neuroblastoma. The present sequence is  
 CC that of a degenerate DNA sequence which is related to the invention.  
 XX  
 SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;  
 Query Match 100.0%; Score 10; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCWCWGYYY 10  
 DB 20 RRCWCWGYYY 11  
 RESULT 23  
 AAZ51677  
 ID AAZ51677 standard; DNA; 21 BP.  
 XX  
 AC AAZ51677;  
 XX  
 DT 21-JUN-2000 (first entry)  
 DE  
 XX Human p53 binding consensus sequence.  
 DE  
 XX PRG; p53 target; human; p53-responsive element; cell proliferation;  
 KW consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;  
 KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;  
 KW cell cycle arrest; modulate; treatment; knockout animal;  
 KW cancer susceptibility; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 11  
 FT /\*tag= a  
 FT /note= "n can be 1-10 nucleotides"  
 FT  
 FT  
 FT  
 FT  
 FT  
 PN WO200012526-A1.  
 XX  
 XX 09-MAR-2000.  
 XX  
 XX 27-AUG-1999; 99WO-US019551.  
 XX  
 XX 28-AUG-1998; 98US-0098251P.  
 XX  
 XX (UYPR-) UNIV PRINCETON.  
 XX  
 XX Horikoshi N, Shenk T;  
 XX WPI; 2000-246724/21.  
 XX  
 XX New p53-inducible isolated nucleic acid molecule including open reading

PT frame encoding human homolog of Drosophila melanogaster peroxidasin,  
 XX useful e.g. in detection and treatment of cancer.  
 XX  
 PS Example 2; Page 78; 83pp; English.  
 XX  
 CC The present sequence is the p53 binding consensus sequence, constructed  
 CC from the five potential p53 responsive elements (A-E), located on PRG  
 CC target molecules. They are modulated on induction by p53 activity. The  
 CC tumour suppressor gene p53, functions as a transcription factor and  
 CC interacts with this responsive element and activates transcription from  
 CC the promoter. PRG sequences are potential targets of p53 regulatory  
 CC activity and are useful for modulation of cellular proliferation. It has  
 CC cytostatic and immunomodulatory activity. PRG polynucleotides, proteins  
 CC and antibodies are useful as diagnostic and therapeutic agents for  
 CC detection and treatment of cancer and other proliferative diseases. The  
 CC gene/cDNA may be used for gene therapy, to restore a gene function  
 CC downstream of p53, that cannot be activated in the p53-deficient tumour  
 CC cell. Antibodies can be used as inducers of cell cycle arrest and/or  
 CC apoptosis. The DNA sequences can be used to generate 'knockout' animals  
 CC as a model of cancer susceptibility  
 XX  
 SQ Sequence 21 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 17 Other;  
 Query Match 100.0%; Score 10; DB 3; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRCWCWGYYY 10  
 DB 1 RRCWCWGYYY 10  
 RESULT 24  
 AAZ51677/c  
 ID AAZ51677 standard; DNA; 21 BP.  
 XX  
 AC AAZ51677;  
 XX  
 DT 21-JUN-2000 (first entry)  
 DE  
 XX Human p53 binding consensus sequence.  
 DE  
 XX PRG; p53 target; human; p53-responsive element; cell proliferation;  
 KW consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;  
 KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;  
 KW cell cycle arrest; modulate; treatment; knockout animal;  
 KW cancer susceptibility; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 11  
 FT /\*tag= a  
 FT /note= "n can be 1-10 nucleotides"  
 FT  
 FT  
 FT  
 FT  
 FT  
 PN WO200012526-A1.  
 XX  
 XX 09-MAR-2000.  
 XX  
 XX 27-AUG-1999; 99WO-US019551.  
 XX  
 XX 28-AUG-1998; 98US-0098251P.  
 XX  
 XX (UYPR-) UNIV PRINCETON.  
 XX  
 XX Horikoshi N, Shenk T;  
 XX WPI; 2000-246724/21.  
 XX  
 XX New p53-inducible isolated nucleic acid molecule including open reading  
 PT frame encoding human homolog of Drosophila melanogaster peroxidasin,  
 PT useful e.g. in detection and treatment of cancer.  
 XX

PS Example 2; Page 78; 83pp; English.

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 CC from the five potential p53 responsive elements (A-E), located on PRG  
 CC target molecules. They are modulated on induction by p53 activity. The  
 CC tumour suppressor gene p53, functions as a transcription factor and  
 CC interacts with this responsive element and activates transcription from  
 CC the promoter. PRG sequences are potential targets of p53 regulatory  
 CC activity and are useful for modulation of cellular proliferation. It has  
 CC cytostatic and immunomodulatory activity. PRG polynucleotides, proteins  
 CC and antibodies are useful as diagnostic and therapeutic agents for  
 CC detection and treatment of cancer and other proliferative diseases. The  
 CC gene/cDNA may be used for gene therapy, to restore a gene function  
 CC downstream of p53, that cannot be activated in the p53-deficient tumour  
 CC cell. Antibodies can be used as inducers of cell cycle arrest and/or  
 CC apoptosis. The DNA sequences can be used to generate 'knockout' animals  
 CC as a model of cancer susceptibility

XX SQ Sequence 21 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 17 Other;

Query Match 100.0%; Score 10; DB 3; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
 Db |||||

21 RRRCWGYYY 12

RESULT 25

AAQ56429  
 ID AAQ56429 standard; DNA; 20 BP.

XX AC AAQ56429;

XX 25-MAR-2003 (revised)

DT 29-JUL-1994 (first entry)

XX E6 consensus negative strand primer WD163.

XX Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 KW detection; assay; genital; ss.

XX Synthetic.

XX US283171-A.

XX 01-FEB-1994.

XX 15-FEB-1991; 91US-00651356.

XX 09-SEP-1988; 88US-00243486.

PR 10-MAR-1989; 89US-00322550.

PR 29-AUG-1989; 89WO-US003747.

XX (UYRP ) UNIV ROCHESTER.

PA (HOFF ) HOFFMANN LA ROCHE INC.

XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX WPI; 1994-048082/06.

XX Detection of genital human papilloma virus - by PCR amplification using  
 PT defined consensus primer pairs.

XX Disclosure; Page 9; 13pp; English.

XX The sequence is that of the human papilloma virus (HPV) E6 consensus  
 CC negative strand primer WD163 which was used in the amplification by PCR  
 CC of HPV DNA. It may be used as part of a simple and rapid assay method for  
 CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003  
 CC to correct PF field.)

SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

Query Match 50.0%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WGWYY 9

Db |||||

11 WGWYY 15

RESULT 26

AAQ56429/c

ID AAQ56429 standard; DNA; 20 BP.

XX AC AAQ56429;

XX 25-MAR-2003 (revised)

DT 29-JUL-1994 (first entry)

XX E6 consensus negative strand primer WD163.

XX Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 KW detection; assay; genital; ss.  
 XX Synthetic.  
 XX US283171-A.  
 XX 01-FEB-1994.  
 XX 15-FEB-1991; 91US-00651356.  
 XX 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 XX (UYRP ) UNIV ROCHESTER.  
 PA (HOFF ) HOFFMANN LA ROCHE INC.

XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX WPI; 1994-048082/06.

XX Detection of genital human papilloma virus - by PCR amplification using  
 PT defined consensus primer pairs.

XX Disclosure; Page 9; 13pp; English.

XX The sequence is that of the human papilloma virus (HPV) E6 consensus  
 CC negative strand primer WD163 which was used in the amplification by PCR  
 CC of HPV DNA. It may be used as part of a simple and rapid assay method for  
 CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003  
 CC to correct PF field.)

XX SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

Query Match 50.0%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRCWW 6

Db |||||

15 RRCWW 11

RESULT 27

AAT44825

ID AAT44825 standard; DNA; 20 BP.

XX AC AAT44825;

XX 25-MAR-2003 (revised)

```

DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD163.
XX
XX Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
XX Synthetic.
OS
XX US5527898-A.
XX
XX 18-JUN-1996.
PD
XX 07-JUN-1995; 95US-00474542.
XX
XX 09-SEP-1988; 88US-00243486.
XX
XX 10-MAR-1989; 89US-00322550.
PR
XX 09-SEP-1989; 89WO-US003747.
PR
XX 14-NOV-1990; 90US-00613142.
PR
XX 20-APR-1993; 93US-00050743.
PR
XX 24-SEP-1993; 93US-00126452.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX
XX Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
PI WPI; 1996-299903/30.
XX
XX Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
XX Disclosure; Col 37-38; 96pp; English.
XX
XX The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;
SQ
Query Match 50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 WGGYY 9
Db 11 WGGYY 15
RESULT 28
AAT44825/c
ID AAT44825 standard; DNA; 20 BP.
XX
XX AAT44825;
AC
XX 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
DT
XX HPV E6 region negative strand primer WD163.
DE
XX Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX

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OS Synthetic.
XX
XX US5527898-A.
XX
XX 18-JUN-1996.
PD
XX 07-JUN-1995; 95US-00474542.
XX
XX 09-SEP-1988; 88US-00243486.
XX
XX 10-MAR-1989; 89US-00322550.
PR
XX 09-SEP-1989; 89WO-US003747.
PR
XX 14-NOV-1990; 90US-00613142.
PR
XX 20-APR-1993; 93US-00050743.
PR
XX 24-SEP-1993; 93US-00126452.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX
XX Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
PI WPI; 1996-299903/30.
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XX Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
XX Disclosure; Col 37-38; 96pp; English.
XX
XX The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;
SQ
Query Match 50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RRCWW 6
Db 15 RRCWW 11
RESULT 29
AAT77998
ID AAT77998 standard; DNA; 20 BP.
XX
XX AAT77998;
AC
XX 25-MAR-2003 (revised)
DT 06-OCT-1997 (first entry)
DT
XX Human papillomavirus E6 negative strand consensus primer WD163.
DE
XX Human; papillomavirus; HPV; primer; amplification; PCR;
KW polymerase chain reaction; E6; negative strand; detection; ss.
XX
XX Synthetic.
OS
XX US5639871-A.
XX
XX 17-JUN-1997.
PD
XX 01-JUN-1995; 95US-00457648.
PP

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XX 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 PA Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX WPI; 1997-332084/30.  
 DR  
 XX New oligo:nucleotide probes for human papilloma-virus - used for  
 PT detecting and typing HPV and for detecting previously unknown HPV types  
 PT and subtypes.  
 PS Disclosure; Col 111-112; 94pp; English.  
 XX The present sequence is a human papillomavirus (HPV) E6 negative strand  
 CC consensus primer. (Updated on 25-MAR-2003 to correct PR field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.)  
 XX SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;  
 Query Match 50.0%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 WNGYY 9  
 Db |||||  
 11 WNGYY 15  
 RESULT 30  
 AAT77998/c  
 ID AAT77998 standard; DNA; 20 BP.  
 XX  
 AC AAT77998;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-OCT-1997 (first entry)  
 XX Human papillomavirus E6 negative strand consensus primer WD163.  
 DE  
 XX Human; papillomavirus; HPV; primer; amplification; PCR;  
 KW polymerase chain reaction; E6; negative strand; detection; ss.  
 XX Synthetic.  
 OS  
 XX US5639871-A.  
 PN  
 XX 17-JUN-1997.  
 PD  
 XX 01-JUN-1995; 95US-00457648.  
 XX  
 PR 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 PA Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX WPI; 1997-332084/30.  
 DR  
 XX New oligo:nucleotide probes for human papilloma-virus - used for

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 PT and subtypes.  
 XX Disclosure; Col 111-112; 94pp; English.  
 XX The present sequence is a human papillomavirus (HPV) E6 negative strand  
 CC consensus primer. (Updated on 25-MAR-2003 to correct PR field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.)  
 XX SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;  
 Query Match 50.0%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RRCWW 6  
 Db |||||  
 15 RRCWW 11  
 RESULT 31  
 ABN87013  
 ID ABN87013 standard; RNA; 16 BP.  
 XX  
 AC ABN87013;  
 XX  
 DT 29-JUL-2002 (first entry)  
 DT  
 XX Histone mRNA stabilising sequence SEQ ID NO:51.  
 DE  
 XX Prodrug ribozyme; ribozyme; SV40; HCV; hepatitis C virus; target;  
 KW Simian virus 40; NS5B; viral infection; antiviral; cytostatic; HBV;  
 KW antiallergic; immunosuppressive; gene therapy; AIDS; hepatitis B virus;  
 KW cancer; leukaemia; genetic defect; allergy; autoimmune disease;  
 KW familial genetic disease; primary genetic disease; ss.  
 XX  
 OS Synthetic.  
 XX WO200014252-A1.  
 PN  
 XX 16-MAR-2000.  
 PD  
 XX 02-SEP-1999; 99WO-JP004767.  
 PF  
 XX 03-SEP-1998; 98JP-00249900.  
 PR  
 XX (SUMU ) SUMITOMO PHARM CO LTD.  
 PA  
 XX Tohdoh N, Yamamoto H, Sudo Y;  
 PI  
 XX WPI; 2000-256997/22.  
 DR  
 XX Novel ribozyme prodrug without RNA-cleaving activity, for use e.g. in  
 PT gene therapy to treat viral infections, cancers and diseases due to  
 PT defective genes.  
 XX Disclosure; Page 96; 116pp; Japanese.  
 XX The present invention describes a gene (I) encoding a ribozyme prodrug  
 CC comprising an intervening sequence removable by splicing, and/or lacking  
 CC RNA-cleaving activity. Also described are: (i) an expression vector  
 CC comprising (I) and preferably further comprising a tissue-specific  
 CC promoter; (ii) a ribozyme prodrug comprising an intervening sequence in  
 CC the ribozyme sequence removable by splicing, and lacking RNA-cleaving  
 CC activity; (iii) a drug composition comprising (I); and (iv) the in vivo  
 CC production of mature ribozyme with RNA-cleaving activity by introducing  
 CC (I) into a eukaryote. (I) has antiviral, cytostatic, antiallergic and  
 CC immunosuppressive activities, and can be used in ribozyme and gene  
 CC therapy. The ribozyme prodrug is useful e.g. in gene therapy,  
 CC particularly for treating viral infections such as AIDS and those due to  
 CC hepatitis B virus (HBV) and hepatitis C virus (HCV), cancers including  
 CC those of the liver, pancreas and colon, and leukaemia, and diseases  
 CC caused by genetic defects such as allergy, autoimmune diseases, familial

CC genetic diseases and primary genetic diseases. The ribozyme prodrug,  
 CC without RNA-cleaving activity, is encoded by a gene with an intervening  
 CC sequence in the ribozyme sequence which can be spliced off in cytoplasm  
 CC to give a functional ribozyme. The present sequence is used in the  
 CC exemplification of the present invention

XX Sequence 16 BP; 1 A; 2 C; 2 G; 0 T; 3 U; 8 Other;  
 SQ

Query Match 40.0%; Score 4; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4  
 ||||  
 Db 12 RRRC 15

RESULT 32  
 ABN87013/c  
 ID ABN87013 standard; RNA; 16 BP.  
 XX  
 AC ABN87013;  
 XX  
 DT 29-JUL-2002 (first entry)  
 XX  
 DE Histone mRNA stabilising sequence SEQ ID NO:51.  
 XX  
 KW Prodrug ribozyme; ribozyme; SV40; HCV; hepatitis C virus; target;  
 KW Simian virus 40; NS5B; viral infection; antiviral; cytostatic; HBV;  
 KW antiallergic; immunosuppressive; gene therapy; AIDS; hepatitis B virus;  
 KW cancer; leukaemia; genetic defect; allergy; autoimmune disease;  
 KW familial genetic disease; primary genetic disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200014252-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 02-SEP-1999; 99WO-JP004767.  
 XX  
 PR 03-SEP-1998; 98JP-00249900.  
 XX  
 PA (SUMU) SUMITOMO PHARM CO LTD.  
 XX  
 PI Tohdoh N, Yamamoto H, Sudo Y;  
 XX  
 DR WPI; 2000-256997/22.  
 XX  
 PT Novel ribozyme prodrug without RNA-cleaving activity, for use e.g. in  
 PT gene therapy to treat viral infections, cancers and diseases due to  
 PT defective genes.  
 PS  
 PS Disclosure; Page 96; 116pp; Japanese.  
 XX  
 CC The present invention describes a gene (I) encoding a ribozyme prodrug  
 CC comprising an intervening sequence removable by splicing, and/or lacking  
 CC RNA-cleaving activity. Also described are: (i) an expression vector  
 CC comprising (i) and preferably further comprising a tissue-specific  
 CC promoter; (ii) a ribozyme prodrug comprising an intervening sequence in  
 CC the ribozyme sequence removable by splicing, and lacking RNA-cleaving  
 CC activity; (iii) a drug composition comprising (I); and (iv) the in vivo  
 CC production of mature ribozyme with RNA-cleaving activity by introducing  
 CC (I) into a eukaryote. (I) has antiviral, cytostatic, antiallergic and  
 CC immunosuppressive activities, and can be used in ribozyme and gene  
 CC therapy. The ribozyme prodrug is useful e.g. in gene therapy,  
 CC particularly for treating viral infections such as AIDS and those due to  
 CC hepatitis B virus (HBV) and hepatitis C virus (HCV), cancers including  
 CC those of the liver, pancreas and colon, and leukaemia, and diseases  
 CC caused by genetic defects such as allergy, autoimmune diseases, familial  
 CC genetic diseases and primary genetic diseases. The ribozyme prodrug,  
 CC without RNA-cleaving activity, is encoded by a gene with an intervening  
 CC sequence in the ribozyme sequence which can be spliced off in cytoplasm

CC to give a functional ribozyme. The present sequence is used in the  
 CC exemplification of the present invention

XX Sequence 16 BP; 1 A; 2 C; 2 G; 0 T; 3 U; 8 Other;  
 SQ

Query Match 40.0%; Score 4; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4  
 ||||  
 Db 5 RRRC 2

RESULT 33  
 ABQ81373  
 ID ABQ81373 standard; DNA; 19 BP.  
 XX  
 AC ABQ81373;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Matrix metalloproteinase sense PCR primer.  
 XX  
 KW Mitogen activated protein kinase; MAPK; signal transduction;  
 KW matrix metalloproteinase; MMP; enzyme; human; invasion-associated gene;  
 KW cytostatic; glioma; cancer; therapy; assay; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200247535-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US047766.  
 XX  
 PR 14-DEC-2000; 2000US-0255548P.  
 XX  
 PA (NYXI-) NYXIS NEURO THERAPIES INC.  
 XX  
 PI Yamamoto H, Moskal J;  
 XX  
 DR WPI; 2002-713241/77.  
 XX  
 PT Identifying a modulator of mitogen-activated protein kinase pathway, by  
 PT contacting a cell transfected with recombinant construct encoding  
 PT reporter gene, with a compound and detecting change in reporter gene  
 PT expression.  
 PS  
 PS Example 1; Page 11; 36pp; English.  
 CC  
 CC The present sequence is that of a degenerate sense PCR primer for human  
 CC matrix metalloproteinase (MMP). Use with the antisense primer given in  
 CC ABQ81374 produces a PCR product of 400 bp. PCR was used to examine  
 CC expression of MMPs in a panel of human brain tumour cell lines. MMP-1 and  
 CC MMP-3 were expressed in SW-1088, U-87MG and U-118 glioma cell lines and  
 CC in SK-N-SH neuroblastoma cells, while D54-MG glioma cells expressed low  
 CC levels of MMP-3 with no MMP-1 expression. Neither MMP-1 nor MMP-3 was  
 CC expressed in U-373 MG or SNB-19, and 3 other neuroblastoma cell lines  
 CC showed no MMP expression. MMP-10 expression was found in SW1088 and U-  
 CC 87MG glioma cell lines. No MMP-10 mRNA expression was found in  
 CC neuroblastoma cell lines. The invention provides a method of identifying  
 CC a compound affecting the mitogen-activated protein kinase (MAPK) pathway.  
 CC This involves contacting a test compound with a cell stably transfected  
 CC with a recombinant construct comprising a reporter gene operatively  
 CC linked to a c-fos promoter, and detecting a change in the expression of  
 CC the reporter gene. The cell constitutively expresses low levels of an  
 CC invasion-associated gene (e.g. MMP), whereby stimulation of the invasion-  
 CC associated gene occurs via activation of the MAPK pathway. Assay systems  
 CC are provided to identify compounds that modulate expression of MMP-1 and  
 CC MMP-3 in cancer cells. Such compounds are useful in cancer therapy

XX Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

```
Query Match      40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 WGY 9
      |||||
Db      6 WGY 9

RESULT 34
ABQ81373/c
ID ABQ81373 standard; DNA; 19 BP.
XX
AC ABQ81373;
XX
DT 12-DEC-2002 (first entry)
XX
DE Matrix metalloproteinase sense PCR primer.
XX
KW Mitogen activated protein kinase; MAPK; signal transduction;
KW matrix metalloproteinase; MMP; enzyme; human; invasion-associated gene;
KW cytotatic; glioma; cancer; therapy; assay; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200247535-A2.
XX
PD 20-JUN-2002.
XX
PF 14-DEC-2001; 2001WO-US047766.
XX
PR 14-DEC-2000; 2000US-0255548P.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Moskal J;
XX
DR WPI; 2002-713241/77.
XX
PT Identifying a modulator of mitogen-activated protein kinase pathway, by
PT contacting a cell transfected with recombinant construct encoding
PT reporter gene, with a compound and detecting change in reporter gene
PT expression.
XX
PS Example 1; Page 11; 36pp; English.
XX
CC The present sequence is that of a degenerate sense PCR primer for human
CC matrix metalloproteinase (MMP). Use with the antisense primer given in
CC ABQ81374 produces a PCR product of 400 bp. PCR was used to examine
CC expression of MMPs in a panel of human brain tumour cell lines. MMP-1 and
CC MMP-3 were expressed in SW-1088, U-87MG and U-118 glioma cell lines and
CC in SK-N-SH neuroblastoma cells, while D54-MG glioma cell lines and
CC levels of MMP-3 with no MMP-1 expression. Neither MMP-1 nor MMP-3 was
CC expressed in U-373 MG or SNB-19, and 3 other neuroblastoma cell lines
CC showed no MMP expression. MMP-10 expression was found in SW1088 and U-
CC 87MG glioma cell lines. No MMP-10 mRNA expression was found in
CC neuroblastoma cell lines. The invention provides a method of identifying
CC a compound affecting the mitogen-activated protein kinase (MAPK) pathway.
CC This involves contacting a test compound with a cell stably transfected
CC with a recombinant construct comprising a reporter gene operatively
CC linked to a c-fos promoter, and detecting a change in the expression of
CC the reporter gene. The cell constitutively expresses low levels of an
CC invasion-associated gene (e.g. MMP), whereby stimulation of the invasion-
CC associated gene occurs via activation of the MAPK pathway. Assay systems
CC are provided to identify compounds that modulate expression of MMP-1 and
CC MMP-3 in cancer cells. Such compounds are useful in cancer therapy
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

Query Match      40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 WGY 9
      |||||
Db      6 WGY 9

RESULT 35
AAD27333/c
ID AAD27333 standard; DNA; 19 BP.
XX
AC AAD27333;
XX
DT 18-APR-2002 (first entry)
XX
DE Human MMP cdna cloning sense RT-PCR primer.
XX
KW Human; cancer; urokinase-type plasminogen activator; uPA; inflammation;
KW Ets-1 transcription factor; N-acetylglucosaminyltransferase V; Gnt-V;
KW matrix-type metalloproteinase; MMP-1; MMP-3; gene therapy; c-ets-1;
KW reverse transcription PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200196606-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019248.
XX
PR 14-JUN-2000; 2000US-00593488.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Kroes R, Moskal JR;
XX
DR WPI; 2002-130746/17.
XX
PT Identifying a compound for treating cancer, comprises detecting
PT transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-
PT type plasminogen activator, matrix-type metalloproteinase-1 and -3 gene
PT expression.
XX
PS Example 1; Page 20; 63pp; English.
XX
CC The invention relates to a method of identifying a compound for treating
CC cancer. The method involves detecting the expression of a panel of
CC sequences selected from transcription factor Ets-1, urokinase-type
CC plasminogen activator (uPA), N-acetylglucosaminyltransferase V (Gnt-V),
CC matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method
CC is useful for identifying a compound that affects a cell, particularly a
CC cancer cell or glioma cell, or a cell that is involved in inflammation.
CC It is used for diagnosing and/or treating cancer or other conditions that
CC are affected by one or more members of a panel of genes or their protein
CC product. The method is also useful for drug discovery, drug safety
CC evaluations and in gene therapy. The present sequence is reverse
CC transcription PCR (RT-PCR) primer used to clone human MMP cdna
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

Query Match      40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 WGY 9
      |||||
Db      6 WGY 9

RESULT 36
AAD27333/c
ID AAD27333 standard; DNA; 19 BP.
XX
AC AAD27333;
```



XX 18-APR-2002 (first entry)  
 XX Human MMP CDNA cloning sense RT-PCR primer.  
 XX  
 XX Human; cancer; urokinase-type plasminogen activator; uPA; inflammation;  
 KW Ets-1 transcription factor; N-acetylglucosaminyltransferase V; Gnt-V;  
 KW matrix-type metalloproteinase; MMP-1; MMP-3; gene therapy; c-ets-1;  
 KW reverse transcription PCR; RT-PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200196606-A2.  
 XX  
 XX 20-DEC-2001.  
 XX  
 XX 14-JUN-2001; 2001WO-US019248.  
 XX  
 XX 14-JUN-2000; 2000US-00593488.  
 XX  
 XX (NYXI-) NYXIS NEURO THERAPIES INC.  
 XX  
 XX Yamamoto H, Kroes R, Moskal JR;  
 XX  
 XX WPI; 2002-130746/17.  
 XX  
 XX Identifying a compound for treating cancer, comprises detecting  
 XX transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-  
 XX type plasminogen activator, matrix-type metalloproteinase-1 and -3 gene  
 XX expression.  
 XX  
 XX Example 1; Page 20; 63pp; English.  
 XX  
 XX The invention relates to a method of identifying a compound for treating  
 XX cancer. The method involves detecting the expression of a panel of  
 XX sequences selected from transcription factor Ets-1, urokinase-type  
 XX plasminogen activator (uPA), N-acetylglucosaminyltransferase V (Gnt-V),  
 XX matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method  
 XX is useful for identifying a compound that affects a cell, particularly a  
 XX cancer cell or glioma cell, or a cell that is involved in inflammation.  
 XX It is used for diagnosing and/or treating cancer or other conditions that  
 XX are affected by one or more members of a panel of genes or their protein  
 XX product. The method is also useful for drug discovery, drug safety  
 XX evaluations and in gene therapy. The present sequence is reverse  
 XX transcription PCR (RT-PCR) primer used to clone human MMP CDNA  
 XX  
 XX Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;  
 XX  
 XX Query Match 40.0%; Score 4; DB 6; Length 19;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 2 RRCW 5  
 XX Db 9 RRCW 6  
 XX  
 XX RESULT 37  
 XX AAQ56430  
 XX ID AAQ56430 standard; DNA; 20 BP.  
 XX  
 XX AC AAQ56430;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 29-JUL-1994 (first entry)  
 XX  
 XX E6 consensus negative strand primer WD164.  
 XX  
 XX Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 XX detection; assay; genital; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX US5283171-A.  
 XX  
 XX 01-FEB-1994.  
 XX  
 XX 15-FEB-1991; 91US-00651356.  
 XX  
 XX 09-SEP-1988; 88US-00243486.  
 XX 10-MAR-1989; 89US-00322550.  
 XX 29-AUG-1989; 89WO-US003747.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.  
 XX  
 XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;  
 XX  
 XX WPI; 1994-048082/06.  
 XX  
 XX Detection of genital human papilloma virus - by PCR amplification using  
 XX defined consensus primer pairs.  
 XX  
 XX Disclosure; Page 9; 13pp; English.  
 XX  
 XX The sequence is that of the human papilloma virus (HPV) E6 consensus  
 XX negative strand primer WD164 which was used in the amplification by PCR  
 XX of HPV DNA. It may be used as part of a simple and rapid assay method for  
 XX detecting and typing HPV in biological samples. (Updated on 25-MAR-2003  
 XX to correct PF field.)  
 XX  
 XX Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;  
 XX  
 XX Query Match 40.0%; Score 4; DB 2; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 6 WGY 9  
 XX Db 12 WGY 15  
 XX  
 XX RESULT 38  
 XX AAQ56430/C  
 XX ID AAQ56430 standard; DNA; 20 BP.  
 XX  
 XX AC AAQ56430;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 29-JUL-1994 (first entry)  
 XX  
 XX E6 consensus negative strand primer WD164.  
 XX  
 XX Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 XX detection; assay; genital; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX US5283171-A.  
 XX  
 XX 01-FEB-1994.  
 XX  
 XX 15-FEB-1991; 91US-00651356.  
 XX  
 XX 09-SEP-1988; 88US-00243486.  
 XX 10-MAR-1989; 89US-00322550.  
 XX 29-AUG-1989; 89WO-US003747.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.  
 XX  
 XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;  
 XX  
 XX WPI; 1994-048082/06.  
 XX  
 XX Detection of genital human papilloma virus - by PCR amplification using

PN US5283171-A.  
 XX  
 XX 01-FEB-1994.  
 XX  
 XX 15-FEB-1991; 91US-00651356.  
 XX  
 XX 09-SEP-1988; 88US-00243486.  
 XX 10-MAR-1989; 89US-00322550.  
 XX 29-AUG-1989; 89WO-US003747.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.  
 XX  
 XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;  
 XX  
 XX WPI; 1994-048082/06.  
 XX  
 XX Detection of genital human papilloma virus - by PCR amplification using  
 XX defined consensus primer pairs.  
 XX  
 XX Disclosure; Page 9; 13pp; English.  
 XX  
 XX The sequence is that of the human papilloma virus (HPV) E6 consensus  
 XX negative strand primer WD164 which was used in the amplification by PCR  
 XX of HPV DNA. It may be used as part of a simple and rapid assay method for  
 XX detecting and typing HPV in biological samples. (Updated on 25-MAR-2003  
 XX to correct PF field.)  
 XX  
 XX Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;  
 XX  
 XX Query Match 40.0%; Score 4; DB 2; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 6 WGY 9  
 XX Db 12 WGY 15  
 XX  
 XX RESULT 38  
 XX AAQ56430/C  
 XX ID AAQ56430 standard; DNA; 20 BP.  
 XX  
 XX AC AAQ56430;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 29-JUL-1994 (first entry)  
 XX  
 XX E6 consensus negative strand primer WD164.  
 XX  
 XX Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 XX detection; assay; genital; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX US5283171-A.  
 XX  
 XX 01-FEB-1994.  
 XX  
 XX 15-FEB-1991; 91US-00651356.  
 XX  
 XX 09-SEP-1988; 88US-00243486.  
 XX 10-MAR-1989; 89US-00322550.  
 XX 29-AUG-1989; 89WO-US003747.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.  
 XX  
 XX Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;  
 XX  
 XX WPI; 1994-048082/06.  
 XX  
 XX Detection of genital human papilloma virus - by PCR amplification using

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PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD164 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRCW 5
Db 15 RRCW 12

RESULT 39
AAQ56428
ID AAQ56428 standard; DNA; 20 BP.
AC AAQ56428;
XX
DT 25-MAR-2003 (revised)
DT 29-JUL-1994 (first entry)
XX
DE E6 consensus negative strand primer WD155.
XX
KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW detection; assay; genital; ss.
XX
OS Synthetic.
XX
FN US283171-A.
XX
PD 01-FEB-1994.
XX
PF 15-FEB-1991; 91US-00651356.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
XX
PA (UYRP ) UNIV ROCHESTER.
PA (HOPF ) HOFFMANN LA ROCHE INC.
XX
PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;
XX WPI; 1994-048082/06.
XX
DR Detection of genital human papilloma virus - by PCR amplification using
PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD155 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RRCW 6
Db 14 RRCW 11

RESULT 41
AAAT44824
ID AAAT44824 standard; DNA; 20 BP.
XX
AC AAAT44824;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD155.
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.

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XX PN US5527898-A.
XX PD 18-JUN-1996.
XX PF 07-JUN-1995; 95US-00474542.
XX PR 09-SEP-1988; 88US-00243486.
XX PR 10-MAR-1989; 89US-00322550.
XX PR 09-SEP-1989; 89WO-US003747.
XX PR 14-NOV-1990; 90US-00613142.
XX PR 20-APR-1993; 93US-00050743.
XX PR 24-SEP-1993; 93US-00126452.
XX PA (HOFF ) HOFFMANN LA ROCHE INC.
XX PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX WPI; 1996-299903/30.
XX Nucleic acid hybridisation probes - specific for selected human papilloma
XX virus types.
XX Disclosure; Col 37-38; 96pp; English.
XX The invention relates to new oligonucleotide probes and primers used for
XX the detection of human papillomaviruses (HPV) which are not genital types
XX 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
XX to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
XX consensus primers and typing probes AAT44733-T44906, which are based on
XX and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
XX sequences. Detection of the amplification prods. is done with probes
XX derived from consensus sequences found in all characterised HPV
XX strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
XX the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
XX are detected using the E6 consensus probes AAT44839-40, specific for
XX these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 WWGY 8
DB 11 WWGY 14
RESULT 42
AAT44824/C
ID AAT44824 standard; DNA; 20 BP.
XX AC AAT44824;
XX DT 25-MAR-2003 (revised)
XX DT 31-JAN-1997 (first entry)
XX DE HPV E6 region negative strand primer WD155.
XX KW Probe; primer; PCR; polymerase chain reaction; amplification;
XX KW human papillomavirus; consensus; ss.
XX OS Synthetic.
XX PN US5527898-A.
XX PR 09-SEP-1988; 88US-00243486.
XX PR 10-MAR-1989; 89US-00322550.
XX PR 09-SEP-1989; 89WO-US003747.
XX PR 14-NOV-1990; 90US-00613142.
XX PR 20-APR-1993; 93US-00050743.
XX PR 24-SEP-1993; 93US-00126452.
XX PF 07-JUN-1995; 95US-00474542.
XX XX

PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX PA (HOFF ) HOFFMANN LA ROCHE INC.
XX PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX WPI; 1996-299903/30.
XX Nucleic acid hybridisation probes - specific for selected human papilloma
XX virus types.
XX Disclosure; Col 37-38; 96pp; English.
XX The invention relates to new oligonucleotide probes and primers used for
XX the detection of human papillomaviruses (HPV) which are not genital types
XX 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
XX to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
XX consensus primers and typing probes AAT44733-T44906, which are based on
XX and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
XX sequences. Detection of the amplification prods. is done with probes
XX derived from consensus sequences found in all characterised HPV
XX strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
XX the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
XX are detected using the E6 consensus probes AAT44839-40, specific for
XX these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RCWW 6
DB 14 RCWW 11
RESULT 43
AAT44826
ID AAT44826 standard; DNA; 20 BP.
XX AC AAT44826;
XX DT 25-MAR-2003 (revised)
XX DT 31-JAN-1997 (first entry)
XX DE HPV E6 region negative strand primer WD164.
XX KW Probe; primer; PCR; polymerase chain reaction; amplification;
XX KW human papillomavirus; consensus; ss.
XX OS Synthetic.
XX PN US5527898-A.
XX PD 18-JUN-1996.
XX PF 07-JUN-1995; 95US-00474542.
XX PR 09-SEP-1988; 88US-00243486.
XX PR 10-MAR-1989; 89US-00322550.
XX PR 09-SEP-1989; 89WO-US003747.
XX PR 14-NOV-1990; 90US-00613142.
XX PR 20-APR-1993; 93US-00050743.
XX PR 24-SEP-1993; 93US-00126452.
XX XX

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PA (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX WPI; 1996-299903/30.
DR
XX Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
PT
XX Disclosure; Col 37-38; 96pp; English.
PS
XX The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGY 9
Db 12 WGY 15

RESULT 44
AAT44826/C
ID AAT44826 standard; DNA; 20 BP.
XX
AC AAT44826;
XX
XX 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
XX HPV E6 region negative strand primer WD164.
DE
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.
XX
XX US5527898-A.
PN
XX
XX 18-JUN-1996.
PD
XX
XX 07-JUN-1995; 95US-00474542.
PF
XX
XX 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
PA
XX
XX Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
PI WPI; 1996-299903/30.
DR
XX Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
PT
XX Disclosure; Col 111-112; 94pp; English.
PS
XX The present sequence is a human papillomavirus (HPV) E6 negative strand
CC

```

CC consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;  
 Query Match 40.0%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 WGGY 8  
 ||||  
 Db 11 WGGY 14

RESULT 46  
 AAT77997/C  
 ID AAT77997 standard; DNA; 20 BP.  
 XX  
 AC AAT77997;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-OCT-1997 (first entry)  
 XX  
 XX Human papillomavirus E6 negative strand consensus primer WD155.  
 XX Human; papillomavirus; HPV; primer; amplification; PCR;  
 KW polymerase chain reaction; E6; negative strand; detection; ss.  
 XX Synthetic.  
 OS  
 XX US5639871-A.  
 XX  
 PD 17-JUN-1997.  
 XX  
 PF 01-JUN-1995; 9SUS-00457648.  
 XX  
 PR 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX  
 PA (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX  
 PI Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX  
 XX WPI; 1997-332084/30.  
 XX  
 PF 01-JUN-1995; 9SUS-00457648.  
 XX  
 PR 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX  
 PA (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX  
 PI Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX  
 XX WPI; 1997-332084/30.  
 XX  
 PT New oligo:nucleotide probes for human papilloma-virus - used for  
 PT detecting and typing HPV and for detecting previously unknown HPV types  
 PT and subtypes.  
 XX  
 PS Disclosure; Col 111-112; 94pp; English.  
 XX  
 CC The present sequence is a human papillomavirus (HPV) E6 negative strand  
 CC consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;  
 Query Match 40.0%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 RCWW 6  
 ||||  
 Db 14 RCWW 11

RESULT 47  
 AAT77999

ID AAT77999 standard; DNA; 20 BP.  
 XX  
 AC AAT77999;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-OCT-1997 (first entry)  
 XX  
 DE Human papillomavirus E6 negative strand consensus primer WD164.  
 XX Human; papillomavirus; HPV; primer; amplification; PCR;  
 KW polymerase chain reaction; E6; negative strand; detection; ss.  
 XX Synthetic.  
 OS  
 XX US5639871-A.  
 XX  
 PD 17-JUN-1997.  
 XX  
 PF 01-JUN-1995; 9SUS-00457648.  
 XX  
 PR 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX  
 PA (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX  
 PI Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX  
 XX WPI; 1997-332084/30.  
 XX  
 PT New oligo:nucleotide probes for human papilloma-virus - used for  
 PT detecting and typing HPV and for detecting previously unknown HPV types  
 PT and subtypes.  
 XX  
 PS Disclosure; Col 111-112; 94pp; English.  
 XX  
 CC The present sequence is a human papillomavirus (HPV) E6 negative strand  
 CC consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;  
 Query Match 40.0%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 WGGY 9  
 ||||  
 Db 12 WGGY 15

RESULT 48  
 AAT77999/C  
 ID AAT77999 standard; DNA; 20 BP.  
 XX  
 AC AAT77999;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-OCT-1997 (first entry)  
 XX  
 DE Human papillomavirus E6 negative strand consensus primer WD164.  
 XX Human; papillomavirus; HPV; primer; amplification; PCR;  
 KW polymerase chain reaction; E6; negative strand; detection; ss.  
 XX Synthetic.  
 OS  
 XX US5639871-A.  
 XX

```

PD 17-JUN-1997.
PF 01-JUN-1995; 9SUS-00457648.
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
PA (HOFF ) ROCHE MOLECULAR SYSTEMS INC.
XX Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
PI Gravitt PE;
XX WPI; 1997-332084/30.
XX New oligo:nucleotide probes for human papilloma-virus - used for
PT detecting and typing HPV and for detecting previously unknown HPV types
PT and subtypes.
XX PS Disclosure; Col 111-112; 94pp; English.
XX CC The present sequence is a human papillomavirus (HPV) E6 negative strand
CC consensus primer. (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RRCW 5
DB 15 RRCW 12
RESULT 49
AAV10231
ID AAV10231 standard; DNA; 20 BP.
XX AC AAV10231;
XX 29-MAY-1998 (first entry)
XX p53 binding DNA consensus sequence.
XX Tumour suppressor; reporter molecule; detection; p53; identification;
XX radiation therapy; biopsy; ss.
XX Homo sapiens.
XX WO9745556-A1.
XX 04-DEC-1997.
XX 09-MAY-1997; 97WO-US006545.
XX 31-MAY-1996; 96US-00657828.
XX (ONYX-) ONYX PHARM INC.
XX Fattaey A;
XX WPI; 1998-041761/04.
XX Determining tumour suppressor status of tumour - via transformation with
XX construct expressing reporter gene if tumour suppressor is present.
XX Example 1; Page 19; 42pp; English.
XX This sequence represents a p53 DNA binding site consensus sequence which
XX is used in an example of a novel method for determining the tumour
XX suppressor status of a tumour. The method involves administering, to the
XX tumour, a novel construct comprising a nucleic acid molecule encoding a
XX reporter molecule and a nucleic acid molecule capable of binding the
XX tumour suppressor, so that binding causes the reporter molecule to be
XX expressed, and determining if the reporter molecule is produced in the
XX tumour. In this example the tumour suppressor is p53, and the method can
XX be used to identify tumours, particularly of the head and neck, suitable
XX for radiation therapy. This method is rapid and can be performed in vivo,
XX eliminating the need for biopsy samples or cell lysis
XX SQ Sequence 20 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 12 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRRC 4
DB 1 RRRRC 4
RESULT 50
AAV10231/c
ID AAV10231 standard; DNA; 20 BP.
XX AC AAV10231;
XX 29-MAY-1998 (first entry)
XX p53 binding DNA consensus sequence.
XX Tumour suppressor; reporter molecule; detection; p53; identification;
XX radiation therapy; biopsy; ss.
XX Homo sapiens.
XX WO9745556-A1.
XX 04-DEC-1997.
XX 09-MAY-1997; 97WO-US006545.
XX 31-MAY-1996; 96US-00657828.
XX (ONYX-) ONYX PHARM INC.
XX Fattaey A;
XX WPI; 1998-041761/04.
XX Determining tumour suppressor status of tumour - via transformation with
XX construct expressing reporter gene if tumour suppressor is present.
XX Example 1; Page 19; 42pp; English.
XX This sequence represents a p53 DNA binding site consensus sequence which
XX is used in an example of a novel method for determining the tumour
XX suppressor status of a tumour. The method involves administering, to the
XX tumour, a novel construct comprising a nucleic acid molecule encoding a
XX reporter molecule and a nucleic acid molecule capable of binding the
XX tumour suppressor, so that binding causes the reporter molecule to be
XX expressed, and determining if the reporter molecule is produced in the
XX tumour. In this example the tumour suppressor is p53, and the method can
XX be used to identify tumours, particularly of the head and neck, suitable
XX for radiation therapy. This method is rapid and can be performed in vivo,
XX eliminating the need for biopsy samples or cell lysis
XX SQ Sequence 20 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 12 Other;
Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRRC 4
DB 1 RRRRC 4

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRC 4
Db 20 RRRRC 17

RESULT 51
ADF44299 standard; DNA; 20 BP.
AC ADF44299;
XX
DT 12-FEB-2004 (first entry)
XX
DE HPV PCR primer E1350L.
XX
KW detection; human papillomavirus; HPV subtype; PCR; primer; ss.
XX
OS Human papillomavirus.
XX
PN JP2002360271-A.
XX
PD 17-DEC-2002.
XX
PF 28-NOV-2001; 2001JP-00362595.
XX
PR 04-MAY-2001; 2001TW-00110785.
XX
PA (KING-) KING CAR FOOD IND CO LTD.
XX
WPI; 2003-600935/57.
XX
Query Match 40.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
Db 6 GYYY 9

RESULT 52
ADF44299/c
ID ADF44299 standard; DNA; 20 BP.
XX
AC ADF44299;
XX
DT 12-FEB-2004 (first entry)
XX
DE HPV PCR primer E1350L.
XX
KW detection; human papillomavirus; HPV subtype; PCR; primer; ss.
XX
OS Human papillomavirus.
XX
```

```
PN JP2002360271-A.
XX
PD 17-DEC-2002.
XX
PF 28-NOV-2001; 2001JP-00362595.
XX
PR 04-MAY-2001; 2001TW-00110785.
XX
PA (KING-) KING CAR FOOD IND CO LTD.
XX
DR WPI; 2003-600935/57.
XX
PT A detecting apparatus and a detecting method for identifying the subtypes
of many species of human papilloma viruses at the same time and a
composition for the detection.
XX
PS Example 2.3.1; SEQ ID NO 656; 166pp; Japanese.
XX
CC This invention describes a novel detecting apparatus for identifying the
subtypes of human papillomaviruses (HPV) contained in a sample which
comprises a carrier which can load sample, a first oligonucleotide loaded
on first part of the carrier and a second oligonucleotide loaded on
second part of carrier, in which first and second oligonucleotides
hybridise with the DNA of the first and the second HPV subtype and can
identify HPV subtype contained in sample at the same time. This sequence
represents a PCR primer used in the method of the invention.
XX
SQ Sequence 20 BP; 6 A; 1 C; 3 G; 3 T; 0 U; 7 Other;

Query Match 40.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRC 4
Db 9 RRRRC 6

RESULT 53
AAH44952
ID AAH44952 standard; DNA; 21 BP.
XX
AC AAH44952;
XX
DT 11-SEP-2003 (revised)
DT 05-SEP-2001 (first entry)
XX
DE HIV Gp41 region specific probe H-E-M&O-1696P.
XX
KW Multiple viral agent detection; human immunodeficiency virus; HIV;
Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;
blood transfusion; blood donation; viral infection; probe; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200136442-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031738.
XX
PR 17-NOV-1999; 99US-0165916P.
XX
PA (JLJJ/) JT J.
PA (MANA/) MANAK M.
PA (WUKK/) WU K.
PA (CHEN/) CHEN X.
PA (YANG/) YANG L.
XX
PI Ji J, Manak M, Wu K, Chen X, Yang L;
XX
DR WPI; 2001-355605/37.
XX
```

PT Simultaneous detection of HIV, HBV and HCV in samples useful to test  
PT donated blood for viral infection comprises amplification of nucleic  
PT acids.  
PS  
XX  
XX Disclosure; Page 14; 51pp; English.  
XX  
CC This invention relates to a method for detecting multiple viral agents in  
CC a sample. The method consists of amplifying nucleic acids from Human  
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B  
CC virus (HBV) using a mixture of primers specific for HIV, HCV HIV-1 type M  
CC and HIV-1 type O and detecting their presence. Included in the invention  
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a  
CC blood or blood product sample. The method can be used to test blood  
CC donated for transfusions for the presence of infection with HIV, HBV or  
CC HCV. The present sequence represents a probe specific for the gp41 region  
CC of HIV, which can be used in the method of the invention. (Updated on 11-  
CC SEP-2003 to standardise OS field)  
XX  
SQ Sequence 21 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 4 Other;  
Query Match 40.0%; Score 4; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RRCW 5  
Db 11 RRCW 14  
|||||  
RESULT 54  
AAH44952/c  
ID AAH44952 standard; DNA; 21 BP.  
XX  
XX AC AAH44952;  
XX  
DT 11-SEP-2003 (revised)  
DT 05-SEP-2001 (first entry)  
XX  
DE HIV Gp41 region specific probe H-E-M6O-1696P.  
XX  
KW Multiple viral agent detection; human immunodeficiency virus; HIV;  
KW Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;  
KW blood transfusion; blood donation; viral infection; probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200136442-A1.  
XX  
XX 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-US031738.  
XX  
PR 17-NOV-1999; 99US-0165916P.  
XX  
XX (JLJ/J) JI J.  
PA (MANA/) MANAK M.  
PA (WUKK/) WU K.  
PA (CHEN/) CHEN X.  
PA (YANG/) YANG L.  
XX  
XX Ji J, Manak M, Wu K, Chen X, Yang L;  
PI WPI; 2001-355605/37.  
XX  
XX Simultaneous detection of HIV, HBV and HCV in samples useful to test  
XX donated blood for viral infection comprises amplification of nucleic  
XX acids.  
XX  
XX Disclosure; Page 14; 51pp; English.  
XX  
CC This invention relates to a method for detecting multiple viral agents in  
CC a sample. The method consists of amplifying nucleic acids from Human  
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B

CC virus (HBV) using a mixture of primers specific for HBV, HCV HIV-1 type M  
CC and HIV-1 type O and detecting their presence. Included in the invention  
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a  
CC blood or blood product sample. The method can be used to test blood  
CC donated for transfusions for the presence of infection with HIV, HBV or  
CC HCV. The present sequence represents a probe specific for the gp41 region  
CC of HIV, which can be used in the method of the invention. (Updated on 11-  
CC SEP-2003 to standardise OS field)  
XX  
SQ Sequence 21 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 4 Other;  
Query Match 40.0%; Score 4; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 WGYV 9  
Db 14 WGYV 11  
|||||  
RESULT 55  
ADA50047  
ID ADA50047 standard; DNA; 25 BP.  
XX  
XX AC ADA50047;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Pig cDNA encoding cytotoxic T lymphocyte A4 degenerate PCR primer #1.  
XX  
KW Immunosuppressive; cellular immune response; humoral immune response;  
KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;  
KW transplant rejection; ss; PCR; human; primer; rabbit; cow.  
XX  
OS Homo sapiens.  
OS Oryctolagus cuniculus.  
OS Bos taurus.  
XX  
XX US2003086940-A1.  
XX  
XX 08-MAY-2003.  
XX  
PF 20-AUG-2002; 2002US-00225519.  
XX  
PR 10-AUG-2001; 2001US-00928267.  
XX  
XX (COST/) COSTA C.  
PA (PIZZ/) PIZZOLATO M.  
PA (FODG/) FODOR W.  
XX  
XX Costa C, Pizzolato M, Fodor W;  
XX WPI; 2003-625623/59.  
XX  
XX New chimeric proteins comprising a first domain and a second domain  
XX capable of inhibiting a cellular and humoral immune response,  
XX respectively, useful for regulating humoral and cellular effector  
XX functions of the immune system.  
XX  
XX Example 2; Page 9; 59pp; English.  
XX  
XX The invention relates to a chimaeric protein comprising a first domain  
XX capable of inhibiting a cellular immune response and a second domain  
XX capable of inhibiting a humoral immune response. Also included are a  
XX chimaeric DNA construct (comprising a DNA sequence encoding a domain  
XX capable of inhibiting a cellular immune response and a DNA sequence  
XX encoding a domain capable of inhibiting a humoral immune response), a  
XX cloning vector comprising the DNA construct, a host cell transformed by  
XX the vector, a transgenic cell, tissue, organ or mammal comprising the  
XX chimaeric protein, producing a mammal, mammalian organ, tissue or cells,  
XX where the mammal is useful as an organ donor for a human or organ, tissue  
XX or cells transplant into a human, by inserting a nucleic acid encoding a  
XX chimaeric protein defined above into the mammal, organ, tissue or cells,



CC where the protein is expressed in the mammal, organ, tissue or cells,  
 CC defined regions of the DNA appearing as ADA50036 which encodes the pig  
 CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined  
 CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in  
 CC the protection of the porcine cell after xenotransplantation into a  
 CC human, and in inhibiting humoral and cellular defence mechanism.  
 CC Chimaeras were produced comprising pig CTLA4 (cellular immune response  
 CC region) and human CD59 (humoral response region), and of CTLA4 and human  
 CC DAF (not defined). The present sequence is a degenerate PCR primer used  
 CC to isolate the cDNA encoding pig CTLA4.

XX Sequence 25 BP; 2 A; 6 C; 6 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10  
 Db 19 GYYY 22  
 ||||  
 ||||

#### RESULT 56

ADA50047/c  
 ID ADA50047 standard; DNA; 25 BP.

XX ADA50047;

AC ADA50047;

DT 20-NOV-2003 (first entry)

DE Pig cDNA encoding cytotoxic T lymphocyte A4 degenerate PCR primer #1.  
 XX Immunosuppressive; cellular immune response; humoral immune response;  
 KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;  
 KW transplant rejection; ss; PCR; human; primer; rabbit; cow.

OS Homo sapiens.

OS Oryctolagus cuniculus.

OS Bos taurus.

XX US2003086940-A1.

XX 08-MAY-2003.

XX 20-AUG-2002; 2002US-00225519.

XX 10-AUG-2001; 2001US-00928267.

XX (COST/) COSTA C.

PA (PIZZ/) PIZZOLATO M.

PA (FODO/) FODOR W.

XX Costa C, Pizzolato M, Fodor W;

XX WPI; 2003-625623/59.

XX New chimeric proteins comprising a first domain and a second domain  
 CC capable of inhibiting a cellular and humoral immune response,  
 PT respectively, useful for regulating humoral and cellular effector  
 PT functions of the immune system.

XX Example 2; Page 9; 59pp; English.

XX The invention relates to a chimaeric protein comprising a first domain  
 CC capable of inhibiting a cellular immune response and a second domain  
 CC capable of inhibiting a humoral immune response. Also included are a  
 CC chimaeric DNA construct (comprising a DNA sequence encoding a domain  
 CC capable of inhibiting a cellular immune response and a DNA sequence  
 CC encoding a domain capable of inhibiting a humoral immune response), a  
 CC cloning vector comprising the DNA construct, a host cell transformed by  
 CC the vector, a transgenic cell, tissue, organ or mammal comprising the  
 CC chimaeric protein, producing a mammal, mammalian organ, tissue or cells,  
 CC where the mammal is useful as an organ donor for a human or organ, tissue

CC or cells transplant into a human, by inserting a nucleic acid encoding a  
 CC chimaeric protein defined above into the mammal, organ, tissue or cells,  
 CC where the protein is expressed in the mammal, organ, tissue or cells,  
 CC defined regions of the DNA appearing as ADA50036 which encodes the pig  
 CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined  
 CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in  
 CC the protection of the porcine cell after xenotransplantation into a  
 CC human, and in inhibiting humoral and cellular defence mechanism.  
 CC Chimaeras were produced comprising pig CTLA4 (cellular immune response  
 CC region) and human CD59 (humoral response region), and of CTLA4 and human  
 CC DAF (not defined). The present sequence is a degenerate PCR primer used  
 CC to isolate the cDNA encoding pig CTLA4.

SQ Sequence 25 BP; 2 A; 6 C; 6 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRC 4  
 Db 22 RRRRC 19  
 ||||  
 ||||

#### RESULT 57

AAZ57335

ID AAZ57335 standard; DNA; 26 BP.

XX AAZ57335;

AC AAZ57335;

DT 03-APR-2000 (first entry)

DE TRH-producing microbe detection oligonucleotide probe.

XX Thermostable direct haemolysin; TDH; TDH-related haemolysin; TRH;

KW Vibrio parahaemolyticus; detection; probe; ss.

OS Vibrio parahaemolyticus.

XX JPI11318480-A.

XX 24-NOV-1999.

XX 15-MAY-1990; 99JP-00106870.

XX 15-MAY-1990; 90JP-00124612.

XX (TOYM ) TOYOH K.

XX WPI; 2000-100773/09.

XX An oligonucleotide for the detection of Vibrio parahaemolyticus -  
 PT provides highly specific detection.

XX Claim 1; Page 2; 6pp; Japanese.

XX The present sequence represents an oligonucleotide which can be used for  
 CC the detection of a TRH-producing microbe (where TRH is a TDH-related  
 CC haemolysin, and TDH is thermostable direct haemolysin). The  
 CC oligonucleotide is useful for detection of Vibrio parahaemolyticus. The  
 CC oligonucleotide provides highly specific detection

SQ Sequence 26 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 3; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRC 4  
 Db 6 RRRRC 9  
 ||||  
 ||||

```

RESULT 58
AAZ57335/c
ID AAZ57335 standard; DNA; 26 BP.
XX
AC AAZ57335;
XX
DT 03-APR-2000 (first entry)
XX
DE TRH-producing microbe detection oligonucleotide probe.
XX
KW Thermostable direct haemolysin; TDH; TDH-related haemolysin; TRH;
KW Vibrio parahaemolyticus; detection; probe; ss.
XX
OS Vibrio parahaemolyticus.
XX
PN JP11318480-A.
XX
PD 24-NOV-1999.
XX
PF 15-MAY-1990; 99JP-00106870.
XX
PR 15-MAY-1990; 90JP-00124612.
XX
PA (TOYM ) TOYORO KK.
XX
DR WPI; 2000-100773/09.
XX
PT An oligonucleotide for the detection of Vibrio parahaemolyticus -
PT provides highly specific detection.
XX
PS Claim 1; Page 2; 6pp; Japanese.
XX
CC The present sequence represents an oligonucleotide which can be used for
CC the detection of a TRH-producing microbe (where TRH is a TDH-related
CC haemolysin, and TDH is thermostable direct haemolysin). The
CC oligonucleotide is useful for detection of Vibrio parahaemolyticus. The
CC oligonucleotide provides highly specific detection
XX
SQ Sequence 26 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
Db 9 GYYY 6

RESULT 59
AAQ24776
ID AAQ24776 standard; DNA; 27 BP.
XX
AC AAQ24776;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1992 (first entry)
XX
DE Arbitrary PCR primer #7.
XX
KW abitrarily primed polymerase chain reaction; fingerprint; identification;
KW restriction fragment length polymorphisms; RFLP; ss.
XX
OS Synthetic.
XX
PN WO9207095-A1.
XX
PD 30-APR-1992.
XX
PF 15-OCT-1991; 91WO-US007713.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.

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XX (STRA-) STRATAGENE.
XX PA McClelland M, Welsh JT, Sorge JA;
XX PI WPI; 1992-167173/20.
XX DR
XX PT Arbitrarily primed polymerase chain reaction method - allows distinction
XX of bacterial, mammalian and plant species due to individual specific
XX fingerprints produced.
XX PS Claim 5; Page 55; 75pp; English.
XX
CC This sequence is the pUC sequencing primer, which is being claimed as an
CC "arbitrary PCR primer" for use in an arbitrarily primed PCR reaction (AP-
CC PCR). The use of a single primer at low stringency conditions forms
CC primed nucleic acids with a substantial degree of mismatching having
CC occurred between primer and target. Several rounds of PCR are then
CC performed, reproducibly generating specific discrete products that can be
CC resolved into a manageable number of individual bands providing a
CC "fingerprint" of the template DNA. Used against genomic DNA from
CC microorganisms, this method will generate a fingerprint of the organism
CC concerned, thus giving a rapid and simple method of identification and
CC classification. Only a small amount of biological material is required, or
CC and prior knowledge of the nucleotide sequence, molecular biology, or
CC biochemistry of the organism is not necessary. Only one primer is
CC required for amplification/identification. The method may also be used to
CC generate detectable polymorphisms for genetic mapping of animals and
CC humans. See also AAQ24770-7 (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4
Db 15 RRRRC 18

RESULT 60
AAQ24776/c
ID AAQ24776 standard; DNA; 27 BP.
XX
AC AAQ24776;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1992 (first entry)
XX
DE Arbitrary PCR primer #7.
XX
KW abitrarily primed polymerase chain reaction; fingerprint; identification;
KW restriction fragment length polymorphisms; RFLP; ss.
XX
OS Synthetic.
XX
PN WO9207095-A1.
XX
PD 30-APR-1992.
XX
PF 15-OCT-1991; 91WO-US007713.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
XX
PA (STRA-) STRATAGENE.
XX
PI McClelland M, Welsh JT, Sorge JA;
XX DR WPI; 1992-167173/20.
XX
PT Arbitrarily primed polymerase chain reaction method - allows distinction

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PT of bacterial, mammalian and plant species due to individual specific  
 PT fingerprints produced.  
 XX  
 PS Claim 5; Page 55; 75pp; English.  
 XX  
 CC This sequence is the pUC sequencing primer, which is being claimed as an  
 CC "arbitrary PCR primer" for use in an arbitrarily primed PCR reaction (AP-  
 CC PCR). The use of a single primer at low stringency conditions forms  
 CC primed nucleic acids with a substantial degree of mismatching having  
 CC occurred between primer and target. Several rounds of PCR are then  
 CC performed, reproducibly generating specific discrete products that can be  
 CC resolved into a manageable number of individual bands providing a  
 CC "fingerprint" of the template DNA. Used against genomic DNA from  
 CC microorganisms, this method will generate a fingerprint of the organism  
 CC concerned, thus giving a rapid and simple method of identification and  
 CC classification. Only a small amount of biological material is required,  
 CC and prior knowledge of the nucleotide sequence, molecular biology, or  
 CC biochemistry of the organism is not necessary. Only one primer is  
 CC required for amplification/identification. The method may also be used to  
 CC generate detectable polymorphisms for genetic mapping of animals and  
 CC humans. See also AAQ24770-7 (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
 ||||  
 Db 18 GYYY 15

RESULT 61  
 AAT16364  
 ID AAT16364 standard; DNA; 27 BP.  
 XX  
 AC AAT16364;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1996 (first entry)  
 XX  
 DE AP-PCR KpnR associated primer #2.  
 XX  
 KW Primer; arbitrarily primed polymerase chain reaction; AP-PCR;  
 KW amplification; identification; classification; bacteria; mammal; plant;  
 KW polymorphism; genetic mapping; eukaryote; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5487985-A.  
 XX  
 PD 30-JAN-1996.  
 XX  
 PF 09-OCT-1992; 92US-00959119.  
 XX  
 PR 15-OCT-1990; 90US-00598913.  
 PR 21-DEC-1990; 90US-00633095.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Sorge JA, McClelland M, Welsh JT;  
 XX  
 DR WPI; 1996-105231/11.  
 XX  
 CC Novel arbitrarily primed polymerase chain reaction - produces a  
 PT fingerprint pattern of bands, useful for identification and  
 PT classification of organisms.  
 XX  
 PS Disclosure; Col 33; 31pp; English.  
 XX  
 CC The sequences given in AAT16358-64 are primers which were used to  
 CC demonstrate the method of the invention. The method of the invention is

CC termed "arbitrarily primed polymerase chain reaction" (AP-PCR) and causes  
 CC the generation of a set of discrete DNA sequences characteristic of a  
 CC genome. The method comprises forming a PCR admixt. by combining in a PCR  
 CC buffer, genomic DNA and at least one primer 10-50 bases in length and  
 CC then subjecting the admixt. to at least one PCR thermocycle. The  
 CC hybridisation step permits the arbitrary priming of the genomic DNA,  
 CC thereby producing a set of discrete DNA segments. The amplification  
 CC products are then contacted with a second primer, which matches the first  
 CC primer except that the second primer has one or more additional bases at  
 CC the 3' terminus, to form a second admixt. This second admixt. is then  
 CC subjected to PCR thermocycles in which the hybridisation does not permit  
 CC formation of primer-template duplexes with a substantial degree of  
 CC mismatch, thereby amplifying a discrete subset of DNA segments. The  
 CC method may be used for the identification and classification of organisms  
 CC such as bacteria, mammals and plants, and for the generation of  
 CC polymorphisms suitable for genetic mapping of eukaryotes. (Updated on 25-  
 CC MAR-2003 to correct PF field.)  
 XX

SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4  
 ||||  
 Db 15 RRRR 18

RESULT 62  
 AAT16364/c  
 ID AAT16364 standard; DNA; 27 BP.  
 XX  
 AC AAT16364;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1996 (first entry)  
 XX  
 DE AP-PCR KpnR associated primer #2.  
 XX  
 KW Primer; arbitrarily primed polymerase chain reaction; AP-PCR;  
 KW amplification; identification; classification; bacteria; mammal; plant;  
 KW polymorphism; genetic mapping; eukaryote; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5487985-A.  
 XX  
 PD 30-JAN-1996.  
 XX  
 PF 09-OCT-1992; 92US-00959119.  
 XX  
 PR 15-OCT-1990; 90US-00598913.  
 PR 21-DEC-1990; 90US-00633095.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Sorge JA, McClelland M, Welsh JT;  
 XX  
 DR WPI; 1996-105231/11.  
 XX  
 CC Novel arbitrarily primed polymerase chain reaction - produces a  
 PT fingerprint pattern of bands, useful for identification and  
 PT classification of organisms.  
 XX  
 PS Disclosure; Col 33; 31pp; English.  
 XX  
 CC The sequences given in AAT16358-64 are primers which were used to  
 CC demonstrate the method of the invention. The method of the invention is  
 CC termed "arbitrarily primed polymerase chain reaction" (AP-PCR) and causes  
 CC the generation of a set of discrete DNA sequences characteristic of a  
 CC genome. The method comprises forming a PCR admixt. by combining in a PCR  
 CC buffer, genomic DNA and at least one primer 10-50 bases in length and

then subjecting the admixt. to at least one PCR thermocycle. The hybridisation step permits the arbitrary priming of the genomic DNA, thereby producing a set of discrete DNA segments. The amplification products are then contacted with a second primer, which matches the first primer except that the second primer has one or more additional bases at the 3' terminus, to form a second admixt. This second admixt. is then subjected to PCR thermocycles in which the hybridisation does not permit formation of primer-template duplexes with a substantial degree of mismatch, thereby amplifying a discrete subset of DNA segments. The method may be used for the identification and classification of organisms such as bacteria, mammals and plants, and for the generation of polymorphisms suitable for genetic mapping of eukaryotes. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;  
 Query Match 40.0%; Score 4; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 10  
 ||||  
 Db 18 GYY 15

RESULT 63  
 AAZ40324  
 ID AAZ40324 standard; DNA; 27 BP.

AC AAZ40324;

DT 25-FEB-2000 (first entry)

DE PCR primer TYKI-13 for tyrosine kinase coding sequence.

KW PCR primer; tyrosine kinase; RAGE; human; gene expression analysis;  
 KW restriction analysis of gene expression; cancer; tumour tissue;  
 KW drug screening; cell biology; development; oncogenesis;  
 KW gene family member identification; marker gene identification; ss.

OS Synthetic.

OS Homo sapiens.

PN W09957324-A1.

XX 11-NOV-1999.

XX 06-MAY-1999; 99WO-US009898.

XX 06-MAY-1998; 98US-00073407.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Robinson DR, Kung H;

XX WPI; 2000-052982/04.

Restriction analysis of gene expression for characterizing expression in different samples, identifying resistance markers, etc.,.

Example 2; Page 37; 80pp; English.

This sequence represents a PCR primer for restriction analysis of gene expression (RAGE) for human tyrosine kinase coding sequence. The invention relates to a method for the amplification of a sample using two primers which are at least partially complementary to two conserved regions, separated by a defined maximum and minimum distance in each gene. The method is used for analysing expressed genes in biological samples especially two mRNA containing samples and thus different samples can be compared (e.g. cancer and non-cancer samples) to identify differentially expressed genes. RAGE on tyrosine kinase family in normal and tumour tissue blocks showed elevated kinase (NYK and CSK) expression in tumour

CC samples compared to normal. The method also determines the effects of factors like growth factors, cytokines, or hormones and drugs on the gene expression and is also used in drug screening. The method can be utilised for understanding many processes in normal cell biology, development and oncogenesis. Many unidentified gene family members and the full length gene corresponding to the sample can be identified and characterised. It also provides means of identifying predictive marker genes for a given condition. The method utilises smaller amounts of starting material than non-PCR based technologies and it does not require the cloning and sequencing of amplified products, thereby immediate, unambiguous signals produced by known genes and unknown genes is identified. It is sensitive (expression levels of genes transcripts which is 1 out of 2 million can be identified). It is not labour-intensive, time-consuming and analyzes specific gene families rather than all expressed genes. Parallel processing of larger number of samples simultaneously is achieved and the method can be utilised on multiple automated devices which measures the expression levels of thousands of genes in hundreds of samples

Sequence 27 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 7 Other;

Query Match 40.0%; Score 4; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWGY 8  
 ||||  
 Db 16 WWGY 19

RESULT 64

AAZ40324/c

ID AAZ40324 standard; DNA; 27 BP.

XX AAZ40324;

XX 25-FEB-2000 (first entry)

DE PCR primer TYKI-13 for tyrosine kinase coding sequence.

KW PCR primer; tyrosine kinase; RAGE; human; gene expression analysis;  
 KW restriction analysis of gene expression; cancer; tumour tissue;  
 KW drug screening; cell biology; development; oncogenesis;  
 KW gene family member identification; marker gene identification; ss.

OS Synthetic.

OS Homo sapiens.

PN W09957324-A1.

XX 11-NOV-1999.

XX 06-MAY-1999; 99WO-US009898.

XX 06-MAY-1998; 98US-00073407.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Robinson DR, Kung H;

XX WPI; 2000-052982/04.

Restriction analysis of gene expression for characterizing expression in different samples, identifying resistance markers, etc.,.

Example 2; Page 37; 80pp; English.

This sequence represents a PCR primer for restriction analysis of gene expression (RAGE) for human tyrosine kinase coding sequence. The invention relates to a method for the amplification of a sample using two primers which are at least partially complementary to two conserved regions, separated by a defined maximum and minimum distance in each gene. The method is used for analysing expressed genes in biological samples especially two mRNA containing samples and thus different samples can be compared (e.g. cancer and non-cancer samples) to identify differentially expressed genes. RAGE on tyrosine kinase family in normal and tumour tissue blocks showed elevated kinase (NYK and CSK) expression in tumour

CC especially two mRNA containing samples and thus different samples can be  
 CC compared (e.g. cancer and non-cancer samples) to identify differentially  
 CC expressed genes. RAGE on tyrosine kinase family in normal and tumour  
 CC tissue blocks showed elevated kinase (NYK and CSK) expression in tumour  
 CC samples compared to normal. The method also determines the effects of  
 CC factors like growth factors, cytokines, or hormones and drugs on the gene  
 CC expression and is also used in drug screening. The method can be utilised  
 CC for understanding many processes in normal cell biology, development and  
 CC oncogenesis. Many unidentified gene family members and the full length  
 CC gene corresponding to the sample can be identified and characterised. It  
 CC also provides means of identifying predictive marker genes for a given  
 CC condition. The method utilises smaller amounts of starting material than  
 CC non-PCR based technologies and it does not require the cloning and  
 CC sequencing of amplified products, thereby immediate, unambiguous signals  
 CC produced by known genes and unknown genes is identified. It is sensitive  
 CC (expression levels of genes transcripts which is 1 out of 2 million can  
 CC be identified). It is not labour-intensive, time-consuming and analyzes  
 CC specific gene families rather than all expressed genes. Parallel  
 CC processing of larger number of samples simultaneously is achieved and the  
 CC method can be utilised on multiple automated devices which measures the  
 CC expression levels of thousands of genes in hundreds of samples

XX  
 SQ Sequence 27 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 7 Other;

Query Match 40.0%; Score 4; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCWW 6  
 DB 19 RCWW 16

## RESULT 65

AAS04151  
 ID AAS04151 standard; DNA; 27 BP.

AC AAS04151;

DT 29-AUG-2001 (first entry)

DE Degenerate pUC sequencing primer used in AP-PCR.

KW AP-PCR; arbitrarily primed PCR; arbitrary primer; DNA fingerprint;  
 KW rapid organism identification; PCR primer; pUC; ss.

XX Synthetic.

XX US6207810-B1.

XX 27-MAR-2001.

XX 16-NOV-1993; 93US-00154364.

XX 15-OCT-1990; 90US-00598913.

XX 21-DEC-1990; 90US-00633095.

XX 09-OCT-1992; 92US-00959119.

XX (STRA-) STRATAGENE.

XX (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX McClelland M, Welsh JT;

XX WPI; 2001-298945/31.

XX New isolated transforming growth factor-beta1 repressed transcript 1  
 PT polynucleotide useful for distinguishing growth-arrested cells from non-  
 PT growth-arrested cells, and for producing antibodies.

XX Disclosure; Col 4; 48pp; English.

XX The present sequence for degenerate pUC sequencing primer is used in AP-  
 CC PCR (arbitrarily primed PCR). Various arbitrary primers (AAS04145-

CC AAS04151, AAS04154-AAS04180) are described in the invention of a rapid  
 CC method for generating discrete DNA PCR products (characteristic of a  
 CC genome) as a "fingerprint". The AP-PCR method comprises priming the  
 CC target nucleic acid from a genome or cellular RNA preparation with a  
 CC single-stranded primer to form a primed nucleic acid with a substantial  
 CC degree of mismatch between the primer and target sequence. The primed  
 CC sequence is amplified by at least 1 cycle of PCR and the resulting  
 CC product amplified by a second step of PCR of at least 10 cycles. AP-PCR  
 CC is useful for the rapid identification of bacterial species and strains,  
 CC mammals and plants. AP-PCR is useful as it does not require knowledge of  
 CC the nucleotide sequence of the organism to be identified. Transforming  
 CC growth factor (TGF)-beta1 repressed transcript 1 (TRT1) polynucleotide  
 CC (AAS04153) which is associated with arrested cell growth is also  
 CC described. TRT1 is useful for the production of anti-sense RNA capable of  
 CC hybridising to the TRT1 polynucleotide, for producing antibodies, and for  
 CC distinguishing growth-arrested cells from non-growth-arrested cells. The  
 CC sequence for Lf9.5m (AAU02482) which is associated with normal growth of  
 CC ovary cells is also given

SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 4; Length 27;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4

DB 15 RRRR 18

## RESULT 66

AAS04151/c

ID AAS04151 standard; DNA; 27 BP.

AC AAS04151;

DT 29-AUG-2001 (first entry)

DE Degenerate pUC sequencing primer used in AP-PCR.

KW AP-PCR; arbitrarily primed PCR; arbitrary primer; DNA fingerprint;  
 KW rapid organism identification; PCR primer; pUC; ss.

XX Synthetic.

XX US6207810-B1.

XX 27-MAR-2001.

XX 16-NOV-1993; 93US-00154364.

XX 15-OCT-1990; 90US-00598913.

XX 21-DEC-1990; 90US-00633095.

XX 09-OCT-1992; 92US-00959119.

XX (STRA-) STRATAGENE.

XX (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX McClelland M, Welsh JT;

XX WPI; 2001-298945/31.

XX New isolated transforming growth factor-beta1 repressed transcript 1  
 PT polynucleotide useful for distinguishing growth-arrested cells from non-  
 PT growth-arrested cells, and for producing antibodies.

XX Disclosure; Col 4; 48pp; English.

XX The present sequence for degenerate pUC sequencing primer is used in AP-  
 CC PCR (arbitrarily primed PCR). Various arbitrary primers (AAS04145-  
 CC AAS04151, AAS04154-AAS04180) are described in the invention of a rapid  
 CC method for generating discrete DNA PCR products (characteristic of a  
 CC genome) as a "fingerprint". The AP-PCR method comprises priming the

CC target nucleic acid from a genome or cellular RNA preparation with a  
 CC single-stranded primer to form a primed nucleic acid with a substantial  
 CC degree of mismatch between the primer and target sequence. The primed  
 CC sequence is amplified by at least 1 cycle of PCR and the resulting  
 CC product amplified by a second step of PCR of at least 10 cycles. AP-PCR  
 CC is useful for the rapid identification of bacterial species and strains,  
 CC mammals and plants. AP-PCR is useful as it does not require knowledge of  
 CC the nucleotide sequence of the organism to be identified. Transforming  
 CC growth factor (TGF)-beta1 repressed transcript 1 (TRT1) polynucleotide  
 CC (AA504153) which is associated with arrested cell growth is also  
 CC described. TRT1 is useful for the production of anti-sense RNA capable of  
 CC hybridizing to the TRT1 polynucleotide, for producing antibodies, and for  
 CC distinguishing growth-arrested cells from non-growth-arrested cells. The  
 CC sequence for Lp9.5m (AAU02482) which is associated with normal growth of  
 CC ovary cells is also given

XX SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 4; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
 Db 18 GYYY 15  
 ||||  
 ||||

## RESULT 67

ADJ63790  
 ID ADJ63790 standard; DNA; 27 BP.

XX AC ADJ63790;

XX DT 06-MAY-2004 (first entry)

XX DE Primer #2.

XX ss; primer; identification; classification; polymorphism; tissue typing;  
 KW linkage map; restriction fragment length polymorphism; RFLP;  
 KW differential gene expression.

XX OS Synthetic.

XX PN US6696277-B1.

XX PD 24-FEB-2004.

XX PF 01-MAR-1995; 95US-00397335.

XX PR 15-OCT-1990; 90US-00598913.

XX PR 21-DEC-1990; 90US-00633095.

XX PR 09-OCT-1992; 92US-00959119.

XX PA (STPA-) STRATAGENE.

XX PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX PI McClelland M, Welsh JT, Sorge JA;

XX DR WPI; 2004-178457/17.

XX PT Generating discrete set of DNA segments characteristic of sample of  
 PT single-stranded RNA, useful for identification and classification of  
 PT organisms, comprises carrying out arbitrarily primed polymerase chain  
 PT reaction.

XX PS Disclosure; SEQ ID NO 8; 31pp; English.

XX The invention relates to a method of generating a discrete set of DNA  
 CC characteristic of a single-stranded RNA sample. The method is useful for  
 CC generating a discrete set of DNA segments characteristic of a sample of  
 CC single-stranded RNA. The method is useful for identification and  
 CC classification of organisms, for the generation of polymorphisms suitable  
 CC for genetic mapping of eukaryotes, for the identification of tissue and

CC cell types, and for monitoring changes in the state of gene expression of  
 CC a cell or tissue. The method is used to verify the assignment of a  
 CC bacteria to a species. The method is useful in the generation of linkage  
 CC maps and can be correlated with restriction fragment length polymorphisms  
 CC (RFLPs) and other markers. The method is useful for generating detectable  
 CC polymorphisms for use in genetic mapping of animals and humans. The  
 CC method is used to detect differential gene expression within tissues. The  
 CC method is useful for the identification of tissue as in tissue typing and  
 CC the identification of strain polymorphism and to detect changes in the  
 CC cell or tissue, e.g. particular genes respond to a particular agent or  
 CC level of differential gene expression. The method can identify species,  
 CC cell types or tissues rapidly. The method is capable of initiating  
 CC amplification in the presence of a substantial degree of mismatching. The  
 CC method requires only one primer sequence for amplification. The present  
 CC sequence represents a primer.

SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4  
 Db 15 RRRRC 18  
 ||||  
 ||||

## RESULT 68

ADJ63790/C

ID ADJ63790 standard; DNA; 27 BP.

XX AC ADJ63790;

XX DT 06-MAY-2004 (first entry)

XX DE Primer #2.

XX ss; primer; identification; classification; polymorphism; tissue typing;  
 KW linkage map; restriction fragment length polymorphism; RFLP;  
 KW differential gene expression.

XX OS Synthetic.

XX PN US6696277-B1.

XX PD 24-FEB-2004.

XX PF 01-MAR-1995; 95US-00397335.

XX PR 15-OCT-1990; 90US-00598913.

XX PR 21-DEC-1990; 90US-00633095.

XX PR 09-OCT-1992; 92US-00959119.

XX PA (STRA-) STRATAGENE.

XX PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX PI McClelland M, Welsh JT, Sorge JA;

XX DR WPI; 2004-178457/17.

XX PT Generating discrete set of DNA segments characteristic of sample of  
 PT single-stranded RNA, useful for identification and classification of  
 PT organisms, comprises carrying out arbitrarily primed polymerase chain  
 PT reaction.

XX PS Disclosure; SEQ ID NO 8; 31pp; English.

XX The invention relates to a method of generating a discrete set of DNA  
 CC characteristic of a single-stranded RNA sample. The method is useful for  
 CC generating a discrete set of DNA segments characteristic of a sample of  
 CC single-stranded RNA. The method is useful for identification and  
 CC classification of organisms, for the generation of polymorphisms suitable  
 CC for the generation of polymorphisms suitable

CC for genetic mapping of eukaryotes, for the identification of tissue and  
 CC cell types, and for monitoring changes in the state of gene expression of  
 CC a cell or tissue. The method is used to verify the assignment of a  
 CC bacteria to a species. The method is useful in the generation of linkage  
 CC maps and can be correlated with restriction fragment length polymorphisms  
 CC (RFLPs) and other markers. The method is useful for generating detectable  
 CC polymorphisms, for use in genetic mapping of animals and humans. The  
 CC method is used to detect differential gene expression within tissues. The  
 CC method is useful for the identification of tissue as in tissue typing and  
 CC the identification of strain polymorphism and to detect changes in the  
 CC cell or tissue, e.g. particular genes respond to a particular agent or  
 CC treatment. The method will indicate a response to the treatment at the  
 CC level of differential gene expression. The method can identify species,  
 CC cell types or tissues rapidly. The method is capable of initiating  
 CC amplification in the presence of a substantial degree of mismatching. The  
 CC method requires only one primer sequence for amplification. The present  
 CC sequence represents a primer.

XX  
 SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
 Db 18 GYYY 15  
 ||||

## RESULT 69

ADJ63791  
 ID ADJ63791 standard; DNA; 27 BP.

AC ADJ63791;

XX 06-MAY-2004 (first entry)

XX Primer for pUC sequencing.

XX ss; primer; identification; classification; polymorphism; tissue typing;  
 KW linkage map; restriction fragment length polymorphism; RFLP;  
 KW differential gene expression.

XX Synthetic.

XX US6696277-B1.

XX 24-FEB-2004.

XX 01-MAR-1995; 95US-00397335.

XX 15-OCT-1990; 90US-00598913.

PR 21-DEC-1990; 90US-00633095.

PR 09-OCT-1992; 92US-00959119.

XX (STRA-) STRATAGENE.

PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX McClelland M, Welsh JT, Sorge JA;

XX WPI; 2004-178457/17.

XX Generating discrete set of DNA segments characteristic of sample of  
 PT single-stranded RNA, useful for identification and classification of  
 PT organisms, comprises carrying out arbitrarily primed polymerase chain  
 PT reaction.

XX Disclosure; SEQ ID NO 9; 31pp; English.

XX The invention relates to a method of generating a discrete set of DNA  
 CC characteristic of a single-stranded RNA sample. The method is useful for  
 CC generating a discrete set of DNA segments characteristic of a sample of  
 CC single-stranded RNA. The method is useful for identification and

CC classification of organisms, for the generation of polymorphisms suitable  
 CC for genetic mapping of eukaryotes, for the identification of tissue and  
 CC cell types, and for monitoring changes in the state of gene expression of  
 CC a cell or tissue. The method is used to verify the assignment of a  
 CC bacteria to a species. The method is useful in the generation of linkage  
 CC maps and can be correlated with restriction fragment length polymorphisms  
 CC (RFLPs) and other markers. The method is useful for generating detectable  
 CC polymorphisms, for use in genetic mapping of animals and humans. The  
 CC method is used to detect differential gene expression within tissues. The  
 CC method is useful for the identification of tissue as in tissue typing and  
 CC the identification of strain polymorphism and to detect changes in the  
 CC cell or tissue, e.g. particular genes respond to a particular agent or  
 CC treatment. The method will indicate a response to the treatment at the  
 CC level of differential gene expression. The method can identify species,  
 CC cell types or tissues rapidly. The method is capable of initiating  
 CC amplification in the presence of a substantial degree of mismatching. The  
 CC method requires only one primer sequence for amplification. The present  
 CC sequence represents a pUC sequencing primer.

XX  
 SQ Sequence 27 BP; 4 A; 7 C; 8 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4  
 Db 15 RRRRC 18  
 ||||

## RESULT 70

ADJ63791/c  
 ID ADJ63791 standard; DNA; 27 BP.

XX ADJ63791;

XX 06-MAY-2004 (first entry)

XX Primer for pUC sequencing.

XX ss; primer; identification; classification; polymorphism; tissue typing;  
 KW linkage map; restriction fragment length polymorphism; RFLP;  
 KW differential gene expression.

XX Synthetic.

XX US6696277-B1.

XX 24-FEB-2004.

XX 01-MAR-1995; 95US-00397335.

XX 15-OCT-1990; 90US-00598913.

PR 21-DEC-1990; 90US-00633095.

PR 09-OCT-1992; 92US-00959119.

XX (STRA-) STRATAGENE.

PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.

XX McClelland M, Welsh JT, Sorge JA;

XX WPI; 2004-178457/17.

XX Generating discrete set of DNA segments characteristic of sample of  
 PT single-stranded RNA, useful for identification and classification of  
 PT organisms, comprises carrying out arbitrarily primed polymerase chain  
 PT reaction.

XX Disclosure; SEQ ID NO 9; 31pp; English.

XX The invention relates to a method of generating a discrete set of DNA  
 CC characteristic of a single-stranded RNA sample. The method is useful for  
 CC generating a discrete set of DNA segments characteristic of a sample of  
 CC single-stranded RNA. The method is useful for identification and

CC single-stranded RNA. The method is useful for identification and  
CC classification of organisms, for the generation of polymorphisms suitable  
CC for genetic mapping of eukaryotes, for the identification of tissue and  
CC cell types, and for monitoring changes in the state of gene expression of a  
CC bacteria to a species. The method is used to verify the assignment of a  
CC maps and can be correlated with restriction fragment length polymorphisms  
CC (RFLPs) and other markers. The method is useful for generating detectable  
CC polymorphisms, for use in genetic mapping of animals and humans. The  
CC method is used to detect differential gene expression within tissues. The  
CC the identification of the identification of tissue as in tissue typing and  
CC cell or tissue, e.g. particular genes respond to detect changes in the  
CC treatment. The method will indicate a response to a particular agent or  
CC level of differential gene expression. The method can identify species,  
CC cell types or tissues rapidly. The method is capable of initiating  
CC amplification in the presence of a substantial degree of mismatching. The  
CC method requires only one primer sequence for amplification. The present  
CC sequence represents a pUC sequencing primer.

XX  
SQ Sequence 27 BP; 4 A; 7 C; 8 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
|||||  
Db 18 GYYY 15

RESULT 71  
AAD46919  
ID AAD46919 standard; DNA; 30 BP.  
AC AAD46919;  
XX  
XX 27-JAN-2003 (first entry)  
DE Histone 3' UTR DNA fragment #1.  
KW Gene expression; transcript stability; drug screening; histone; ds.  
OS Mammalia.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 4  
FT /\*tag= a  
FT /note= "This base can be repeated 20-40 times"  
XX  
XX WO200272844-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 08-MAR-2002; 2002WO-AU000351.  
XX  
XX 09-MAR-2001; 2001US-0274770P.  
XX  
XX (GENE-) GENE STREAM PTY LTD.  
XX  
XX Daly J;  
XX  
XX WPI; 2002-759847/82.  
XX  
XX New expression vector useful for modulating gene expression, identifying  
XX and analyzing regulatory sequences, new targets and reagents for treating  
XX human diseases, comprises a transcribable polynucleotide encoding an RNA  
XX element.  
XX  
XX Claim 11; Page 68; 103pp; English.  
XX  
XX The present invention relates to novel expression vectors and/or reporter  
XX vectors providing kinetics of protein expression with improved temporal

CC correlation to the promoter activity. The expression vectors comprise  
CC transcribable polynucleotides having sequences of nucleotides encoding  
CC RNA elements which modulates the stability of a transcript corresponding  
CC to the transcribable polynucleotide. The expression vectors are useful  
CC for modulating the stability of a transcript and determining expression  
CC of a polynucleotide of interest. They are useful for modulating gene  
CC expression, identifying and analysing regulatory sequences, new targets  
CC and reagents for treating human diseases and for drug screening. The  
CC present sequence is histone 3' untranslated region (UTR) DNA fragment.  
XX This sequence is used in the exemplification of the invention

XX  
SQ Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4  
|||||  
Db 21 RRRR 24

RESULT 72  
AAD46919/c  
ID AAD46919 standard; DNA; 30 BP.  
XX  
AC AAD46919;  
XX  
XX 27-JAN-2003 (first entry)  
DE Histone 3' UTR DNA fragment #1.  
KW Gene expression; transcript stability; drug screening; histone; ds.  
XX  
OS Mammalia.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 4  
FT /\*tag= a  
FT /note= "This base can be repeated 20-40 times"  
XX  
XX WO200272844-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 08-MAR-2002; 2002WO-AU000351.  
XX  
XX 09-MAR-2001; 2001US-0274770P.  
XX  
XX (GENE-) GENE STREAM PTY LTD.  
XX  
XX Daly J;  
XX  
XX WPI; 2002-759847/82.  
XX  
XX New expression vector useful for modulating gene expression, identifying  
XX and analyzing regulatory sequences, new targets and reagents for treating  
XX human diseases, comprises a transcribable polynucleotide encoding an RNA  
XX element.  
XX  
XX Claim 11; Page 68; 103pp; English.  
XX  
XX The present invention relates to novel expression vectors and/or reporter  
XX vectors providing kinetics of protein expression with improved temporal  
XX correlation to the promoter activity. The expression vectors comprise  
XX transcribable polynucleotides having sequences of nucleotides encoding  
XX RNA elements which modulates the stability of a transcript corresponding  
XX to the transcribable polynucleotide. The expression vectors are useful  
XX for modulating the stability of a transcript and determining expression  
XX of a polynucleotide of interest. They are useful for modulating gene  
XX expression, identifying and analysing regulatory sequences, new targets  
XX and reagents for treating human diseases and for drug screening. The  
XX present sequence is histone 3' untranslated region (UTR) DNA fragment.



CC This sequence is used in the exemplification of the invention

XX Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 9 Other;  
SQ Query Match 40.0%; Score 4; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4

DB 14 RRCR 11

RESULT 73

AAD46937

ID AAD46937 standard; DNA; 30 BP.

XX AC AAD46937;

XX DT 27-JAN-2003 (first entry)

XX DE Histone 3' UTR DNA fragment #2.

XX KW Gene expression; transcript stability; drug screening; histone;

XX KW DNA-RNA hybrid; ds.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT misc\_feature 4

FT /\*tag= a

FT /note= "This base can be repeated 20-40 times"

FT 15. .18

FT /\*tag= b

FT /label= RNA

XX WO200272844-A1.

XX 19-SEP-2002.

XX 08-MAR-2002; 2002WO-AU000351.

XX 09-MAR-2001; 2001US-0274770P.

XX (GENE-) GENE STREAM PTY LTD.

XX Daly J;

XX WPI; 2002-759847/82.

XX New expression vector useful for modulating gene expression, identifying

XX PT and analyzing regulatory sequences, new targets and reagents for treating

XX PT human diseases, comprises a transcribable polynucleotide encoding an RNA

XX PT element.

XX Example 15; Page 68; 103pp; English.

XX The present invention relates to novel expression vectors and/or reporter

XX CC vectors providing kinetics of protein expression with improved temporal

XX CC correlation to the promoter activity. The expression vectors comprise

XX CC transcribable polynucleotides having sequences of nucleotides encoding

XX CC RNA elements which modulates the stability of a transcript corresponding

XX CC to the transcribable polynucleotide. The expression vectors are useful

XX CC for modulating the stability of a transcript and determining expression

XX CC of a polynucleotide of interest. They are useful for modulating gene

XX CC expression, identifying and analyzing regulatory sequences, new targets

XX CC and reagents for treating human diseases and for drug screening. The

XX CC present sequence is histone 3' untranslated region (UTR) DNA fragment.

XX This sequence is used in the exemplification of the invention

XX SQ Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRCR 4  
DB 21 RRCR 24

RESULT 74

AAD46937/c

ID AAD46937 standard; DNA; 30 BP.

XX AC AAD46937;

XX DT 27-JAN-2003 (first entry)

XX DE Histone 3' UTR DNA fragment #2.

XX KW Gene expression; transcript stability; drug screening; histone;

XX KW DNA-RNA hybrid; ds.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT misc\_feature 4

FT /\*tag= a

FT /note= "This base can be repeated 20-40 times"

FT 15. .18

FT /\*tag= b

FT /label= RNA

XX WO200272844-A1.

XX 19-SEP-2002.

XX 08-MAR-2002; 2002WO-AU000351.

XX 09-MAR-2001; 2001US-0274770P.

XX (GENE-) GENE STREAM PTY LTD.

XX Daly J;

XX WPI; 2002-759847/82.

XX New expression vector useful for modulating gene expression, identifying

XX PT and analyzing regulatory sequences, new targets and reagents for treating

XX PT human diseases, comprises a transcribable polynucleotide encoding an RNA

XX PT element.

XX Example 15; Page 68; 103pp; English.

XX The present invention relates to novel expression vectors and/or reporter

XX CC vectors providing kinetics of protein expression with improved temporal

XX CC correlation to the promoter activity. The expression vectors comprise

XX CC transcribable polynucleotides having sequences of nucleotides encoding

XX CC RNA elements which modulates the stability of a transcript corresponding

XX CC to the transcribable polynucleotide. The expression vectors are useful

XX CC for modulating the stability of a transcript and determining expression

XX CC of a polynucleotide of interest. They are useful for modulating gene

XX CC expression, identifying and analyzing regulatory sequences, new targets

XX CC and reagents for treating human diseases and for drug screening. The

XX CC present sequence is histone 3' untranslated region (UTR) DNA fragment.

XX This sequence is used in the exemplification of the invention

XX SQ Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 3 U; 9 Other;

Query Match 40.0%; Score 4; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4

DB 14 RRCR 11

```

Db      14 RRRRC 11

RESULT 75
AAQ30066
ID AAQ30066 standard; DNA; 32 BP.
XX
AC AAQ30066;
XX
DT 25-MAR-2003 (revised)
DT 04-APR-1993 (first entry)
XX
DE Sequence of PCR primer VH Bam Back for the variable domain heavy chain
DE (VH) of clone B.
XX
KW Antibody; PCR primer; variable heavy chain; ss.
XX
OS Synthetic.
XX
FN WO9218534-A1.
XX
PD 29-OCT-1992.
XX
PF 23-APR-1992; 92WO-GB000746.
XX
PR 23-APR-1991; 91GB-00008652.
XX
PA (ANTI-) ANTISOMA LTD.
XX
PI Courtenay-Luck NS;
XX
DR WPI; 1992-382045/46.
XX
PT New peptide EPPT (Glu-Pro-Pro-Thr) - selectively binds mucin expressed by
PT epithelial tumours, used for guiding toxins or labels to tumours
PT expressing mucin.
XX
PS Example; Table 1, Page 27; 50pp; English.
XX
CC Clone B is a lymphoblastoid cell line (secreting antibody directed
CC against a tumour-associated mucin mol.) derived from the EBV- transforming
CC and cloning of a patient's peripheral blood B-cells. After DNA isolation,
CC the polymerase chain reaction (PCR) was employed, using oligonucleotide
CC primers specific for the variable light and heavy chains of
CC immunoglobulins (see AAQ30065, AAQ30066). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 32 BP; 6 A; 6 C; 9 G; 5 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWVG 7
Db 31 CWVG 28

RESULT 77
AAV39802
ID AAV39802 standard; cDNA; 38 BP.
XX
AC AAV39802;
XX
DT 28-SEP-1998 (first entry)
XX
DE Oligonucleotide SEQ ID NO:320 from WO9820166.
XX
KW Mass spectrometry; diagnosis; detection; biological sample; infection;
KW genetic disease; chromosomal abnormality; identification; heredity;
KW pathogenic organism; telomerase activity; oncogene mutation;
KW cancer-specific sequence; primer; ss.
XX
OS Synthetic.
XX
PN WO9820166-A2.
XX
PD 14-MAY-1998.
XX
PF 06-NOV-1997; 97WO-US020444.
XX
PR 06-NOV-1996; 96US-00744481.
XX
PR 06-NOV-1996; 96US-00744590.
XX
PR 06-NOV-1996; 96US-00746036.
XX
PR 23-JAN-1997; 96US-00746055.
XX
PR 23-JAN-1997; 97US-00786988.
XX
PR 19-SEP-1997; 97US-00787639.
XX
PR 08-OCT-1997; 97US-00933792.
XX
PR 08-OCT-1997; 97US-00947801.
XX
PA (SEQU-) SEQUENOM INC.

Db      14 RRRRC 11

RESULT 76
AAQ30066/c
ID AAQ30066 standard; DNA; 32 BP.
XX
AC AAQ30066;
XX
DT 25-MAR-2003 (revised)
DT 04-APR-1993 (first entry)
XX
DE Sequence of PCR primer VH Bam Back for the variable domain heavy chain
DE (VH) of clone B.
XX
KW Antibody; PCR primer; variable heavy chain; ss.
XX
OS Synthetic.

```

XX Kostor H, Tang K, Fu D, Siebert CW, Little DP, Higgins GS;  
 PI Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;  
 PI Lough DM;  
 XX WPI; 1998-286975/25.  
 XX Sequencing nucleic acid by mass spectrometric analysis - for detecting  
 PT nucleic acids, telomerase activity, oncogene mutations, or cancer-  
 PT specific sequences, for diagnosis of disease.  
 XX Disclosure; Page 336; 478pp; English.  
 XX A process has been developed for determining the sequence of a target  
 CC nucleic acid. The process comprises: (i) generating at least two  
 CC fragments (F) from the target nucleic acid; and (ii) analysing F by mass  
 CC spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically  
 CC claimed primers for use in the mass spectrometric analysis of the above  
 CC process. The process is used to detect genetic diseases (e.g.  
 CC haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's  
 CC disease, cystic fibrosis and many others) or chromosomal abnormalities  
 CC (or predisposition); infections and cancers; also for establishing  
 CC identity and heredity. Particular applications are diagnosis of  
 CC neuroblastoma, detecting telomerase, determining family relationships and  
 CC HLA compatibility, and in genetic fingerprinting. Compared with known  
 CC methods using MS, this process requires fewer specific reagents and is  
 CC better suited to automation. Extended primers are shorter; primer  
 CC annealing is more efficient and the process allows detection of many  
 CC sequences simultaneously. The present sequence represent an  
 CC oligonucleotide from the present invention, which is not actually  
 CC specified within the specification, only within the sequence listing  
 XX Sequence 38 BP; 10 A; 10 C; 7 G; 8 T; 0 U; 3 Other;  
 SQ Query Match 40.0%; Score 4; DB 2; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 CWVG 7  
 Db 33 CWVG 36  
 RESULT 78  
 AAV39802/c  
 ID AAV39802 standard; cDNA; 38 BP.  
 XX AC AAV39802;  
 XX DT 28-SEP-1998 (first entry)  
 XX DE Oligonucleotide SEQ ID NO:320 from WO9820166.  
 XX Mass spectrometry; diagnosis; detection; biological sample; infection;  
 KW genetic disease; chromosomal abnormality; identification; heredity;  
 KW pathogenic organism; telomerase activity; oncogene mutation;  
 KW cancer-specific sequence; primer; ss.  
 XX OS Synthetic.  
 XX WO9820166-A2.  
 XX PN 14-MAY-1998.  
 XX PD 06-NOV-1997; 97WO-US020444.  
 XX PF 06-NOV-1996; 96US-00744481.  
 XX PR 06-NOV-1996; 96US-00744590.  
 XX PR 06-NOV-1996; 96US-00746036.  
 XX PR 06-NOV-1996; 96US-00746055.  
 XX PR 23-JAN-1997; 97US-00786988.  
 XX PR 23-JAN-1997; 97US-00787639.  
 XX PR 19-SEP-1997; 97US-00833792.

PR 08-OCT-1997; 97US-00947801.  
 XX (SEQU-) SEQUENOM INC.  
 XX Kostor H, Tang K, Fu D, Siebert CW, Little DP, Higgins GS;  
 PI Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;  
 PI Lough DM;  
 XX WPI; 1998-286975/25.  
 XX Sequencing nucleic acid by mass spectrometric analysis - for detecting  
 PT nucleic acids, telomerase activity, oncogene mutations, or cancer-  
 PT specific sequences, for diagnosis of disease.  
 XX Disclosure; Page 336; 478pp; English.  
 XX A process has been developed for determining the sequence of a target  
 CC nucleic acid. The process comprises: (i) generating at least two  
 CC fragments (F) from the target nucleic acid; and (ii) analysing F by mass  
 CC spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically  
 CC claimed primers for use in the mass spectrometric analysis of the above  
 CC process. The process is used to detect genetic diseases (e.g.  
 CC haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's  
 CC disease, cystic fibrosis and many others) or chromosomal abnormalities  
 CC (or predisposition); infections and cancers; also for establishing  
 CC identity and heredity. Particular applications are diagnosis of  
 CC neuroblastoma, detecting telomerase, determining family relationships and  
 CC HLA compatibility, and in genetic fingerprinting. Compared with known  
 CC methods using MS, this process requires fewer specific reagents and is  
 CC better suited to automation. Extended primers are shorter; primer  
 CC annealing is more efficient and the process allows detection of many  
 CC sequences simultaneously. The present sequence represent an  
 CC oligonucleotide from the present invention, which is not actually  
 CC specified within the specification, only within the sequence listing  
 XX Sequence 38 BP; 10 A; 10 C; 7 G; 8 T; 0 U; 3 Other;  
 SQ Query Match 40.0%; Score 4; DB 2; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 CWVG 7  
 Db 36 CWVG 33  
 RESULT 79  
 AAA28440  
 ID AAA28440 standard; DNA; 6 BP.  
 XX AC AAA28440;  
 XX DT 29-AUG-2000 (first entry)  
 XX DE Synthetic promoter conserved domain IIB.  
 XX KW Artificial promoter; strong; weak; transgene expression; plant; ss.  
 XX OS Synthetic.  
 XX PN EP1002869-A1.  
 XX PD 24-MAY-2000.  
 XX PF 25-FEB-1999; 99EP-00301419.  
 XX PR 09-NOV-1998; 98IN-DE003322.  
 XX PA (COUL) CSIR COUNCIL SCI IND RES.  
 XX PI Tuli R, Sawant SV, Singh PK, Gupta SK;  
 XX WPI; 2000-341712/30.

XX New chemically synthesized artificial promoter, useful high level  
PT expression of transgenes in different organisms.  
XX  
XX Claim 6; Page 18; 40pp; English.  
XX  
CC A chemically synthesized promoter can comprise a conserved domain IIB as  
CC shown here for high level expression of genes. Chemically synthesized  
CC artificial promoters are new and comprise a DNA sequence designed for a  
CC targeted level and pattern of gene expression by strategically putting  
CC together several signature sequences identified by sequence alignment and  
CC statistical analysis of a large database constructed for this purpose. A  
CC method for chemically synthesizing an artificial promoter for expressing  
CC genes at a desired level in different organisms is also claimed. The high  
CC level expression in a plant using such an artificial promoter (e.g.  
CC AAA28449) can be measured comprising polyethylene glycol (PEG) mediated  
CC transformation of plant protoplasts as well as biolistic mediated  
CC transformation of plant tissues including root, stem, intact leaf tissue  
CC followed by transient GUS assay to compare with a natural CaMV 35S  
CC promoter showing the desired level of activity. The promoter is useful  
CC for high level expression of transgenes in different organisms and for  
CC testing high level gene expression in plants (claimed). The promoter is  
CC biologically active and is efficient and can be synthesized to express in  
CC even the most complex organisms  
XX  
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 0 U; 4 Other;  
Query Match 30.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWW 6  
DB 1 CWW 3  
RESULT 80  
AAA28440/c  
ID AAA28440 standard; DNA; 6 BP.  
AC AAA28440;  
XX  
XX 29-AUG-2000 (first entry)  
XX  
DE Synthetic promoter conserved domain IIB.  
XX  
XX Artificial promoter; strong; weak; transgene expression; plant; ss.  
XX  
OS Synthetic.  
XX  
XX EP1002869-A1.  
XX  
XX 24-MAY-2000.  
XX  
XX 25-FEB-1999; 99EP-00301419.  
XX  
XX 09-NOV-1998; 98IN-DE003322.  
XX  
XX (COUL) CSIR COUNCIL SCI IND RES.  
XX  
XX Tuli R, Sawant SV, Singh PK, Gupta SK;  
XX WPI; 2000-341712/30.  
XX  
XX New chemically synthesized artificial promoter, useful high level  
XX expression of transgenes in different organisms.  
XX  
XX Claim 6; Page 18; 40pp; English.  
XX  
CC A chemically synthesized promoter can comprise a conserved domain IIB as  
CC shown here for high level expression of genes. Chemically synthesized  
CC artificial promoters are new and comprise a DNA sequence designed for a  
CC targeted level and pattern of gene expression by strategically putting

CC together several signature sequences identified by sequence alignment and  
CC statistical analysis of a large database constructed for this purpose. A  
CC method for chemically synthesizing an artificial promoter for expressing  
CC genes at a desired level in different organisms is also claimed. The high  
CC level expression in a plant using such an artificial promoter (e.g.  
CC AAA28449) can be measured comprising polyethylene glycol (PEG) mediated  
CC transformation of plant protoplasts as well as biolistic mediated  
CC transformation of plant tissues including root, stem, intact leaf tissue  
CC followed by transient GUS assay to compare with a natural CaMV 35S  
CC promoter showing the desired level of activity. The promoter is useful  
CC for high level expression of transgenes in different organisms and for  
CC testing high level gene expression in plants (claimed). The promoter is  
CC biologically active and is efficient and can be synthesized to express in  
CC even the most complex organisms  
XX  
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 0 U; 4 Other;  
Query Match 30.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 WWG 7  
DB 6 WWG 4  
RESULT 81  
ADF42928  
ID ADF42928 standard; DNA; 6 BP.  
XX  
XX ADF42928;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
DE Methylated immunostimulatory oligonucleotide ODN #27 SEQ ID NO:27.  
XX  
XX lipid-methylated nucleic acid formulation; immune response;  
XX lipid-nucleic acid; vaccine; immunostimulant; cytostatic;  
XX antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;  
XX arthritis; immunodeficiency disorder;  
XX methylated immunostimulatory oligonucleotide; ss.  
XX  
XX Synthetic.  
XX  
XX WO2003094963-A2.  
XX  
XX 20-NOV-2003.  
XX  
XX 12-MAY-2003; 2003WO-CA000678.  
XX  
XX 10-MAY-2002; 2002US-0379343P.  
XX  
XX 07-NOV-2002; 2002US-00290545.  
XX  
XX 04-APR-2003; 2003US-0460846P.  
XX  
XX (INEX-) INEX PHARM CORP.  
XX  
XX Tam YK, Semple S, Klimuk S, Chikh G;  
XX WPI; 2004-142698/14.  
XX  
XX Lipid-methylated nucleic acid formulation for stimulating an immune  
XX response in an animal comprises a lipid component and a nucleic acid  
XX component comprising a methylated nucleic acid sequence.  
XX  
XX Disclosure; SEQ ID NO 27; 102pp; English.  
XX  
XX The present invention describes a lipid-methylated nucleic acid  
XX formulation for stimulating an immune response in an animal, comprising a  
XX lipid component and a nucleic acid component which is a methylated  
XX nucleic acid sequence. Also described: (1) an adjuvant comprising a lipid  
XX -nucleic acid (LNA) formulation; (2) a vaccine comprising the LNA  
XX formulation in combination with at least one target antigen; (3)  
XX stimulating an enhanced host immune response to antigenic stimulation,

CC comprising administering to the host the LNA formulation; (4) stimulating  
 CC host dendritic cells in vivo, comprising contacting at least one  
 CC dendritic cell with the lipid-methylated nucleic acid formulation to a  
 CC host; and (5) simultaneously delivering antigenic and adjuvant immune  
 CC stimulation to antigen presenting cells, comprising the administration of  
 CC the LNA formulation associated with a target antigen. The lipid-  
 CC methylation nucleic acid formulation has immunostimulant, cytostatic,  
 CC antiinflammatory and antiarthritic activities, and can be used in  
 CC vaccines, and in gene therapy. The formulation and methods are useful in  
 CC stimulating a host's immune response to antigenic stimulation, or in  
 CC activating and/or expanding dendritic cell populations in response to  
 CC antigenic stimulation. They may be used for treating cancer,  
 CC inflammation, arthritis or immunodeficiency disorders. The present  
 CC sequence represents a methylated immunostimulatory oligonucleotide given  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
 |||  
 Db 1 RRC 3

RESULT 82  
 ADF42928/c  
 ID ADF42928 standard; DNA; 6 BP.

XX AC ADF42928;

XX DT 11-MAR-2004 (first entry)

XX DE Methylated immunostimulatory oligonucleotide ODN #27 SEQ ID NO:27.

XX KW lipid-methylated nucleic acid formulation; immune response;  
 KW lipid-nucleic acid; vaccine; immunostimulant; cytostatic;  
 KW antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;  
 KW arthritis; immunodeficiency disorder;  
 KW methylated immunostimulatory oligonucleotide; ss.

OS Synthetic.

XX FN WO2003094963-A2.

XX PD 20-NOV-2003.

XX PF 12-MAY-2003; 2003WO-CA000678.

XX PR 10-MAY-2002; 2002US-0379343P.

XX PR 07-NOV-2002; 2002US-00290545.

XX PR 04-APR-2003; 2003US-0460646P.

XX PA (INEX-) INEX PHARM CORP.

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 CC inflammation, arthritis or immunodeficiency disorders. The present  
 CC sequence represents a methylated immunostimulatory oligonucleotide given  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
 |||  
 Db 6 RRC 4

RESULT 83  
 ADL35954  
 ID ADL35954 standard; DNA; 6 BP.

XX AC ADL35954;

XX DT 20-MAY-2004 (first entry)

XX DE Non-methylated CpG motif consensus sequence.

XX KW cosmetic; pharmaceutical; epithelial tissue; fabric softener;  
 KW hand washing product; body care product; hair care product; hair dye;  
 KW manual dishwashing product; nonmethylated CpG; antiinflammatory;  
 KW dermatological; antipsoriatic; endocrine; vulnery; immunosuppressive;  
 KW interleukin-6 release inhibitor; interleukin-8 release inhibitor;  
 KW epithelial inflammation; inflammation-induced aging; psoriasis;  
 KW atopic eczema; dry skin; alopecia areata; vitiligo; bullous disease;  
 KW graft versus host; UV-induced skin inflammation; parodontosis; ds.

XX OS Unidentified.

XX PN DE10233994-A1.

XX PD 12-FEB-2004.

XX PF 25-JUL-2002; 2002DE-01033994.

XX PR 25-JUL-2002; 2002DE-01033994.

XX PA (PHEN-) PHENION GMBH & CO KG.

XX DR WPI; 2004-192562/19.

XX CC Cosmetic or pharmaceutical composition for treatment of epithelial  
 CC tissue, especially to combat inflammation, comprises nucleic acids with  
 CC nonmethylated CpG units.

XX PS Claim 8; Page 13; 19pp; German.

XX CC This invention describes a novel cosmetic or pharmaceutical composition  
 CC for treatment of epithelial tissue comprising nucleic acids with  
 CC nonmethylated CpG units. The invention also describes a fabric softener,  
 CC hand washing product, body or hair care product, hair dye or manual  
 CC dishwashing product comprising nucleic acids with nonmethylated CpG  
 CC units. The nucleic acids are 6-10 nucleotides in length and include the

CC sequence 5'-A/GA/GC/GC/TC/T-3'. The nucleic acids are optionally modified  
 CC by replacing phosphodiester linkages with methyl phosphonate,  
 CC phosphoramidate, phosphorothioate or hydroxylamine linkages, by replacing  
 CC ribose with other hexo- or pentopyranoses with 3',5'-carbocyclically  
 CC bridged 2'-deoxyribose derivatives or by replacing sugar phosphate units  
 CC with carboxamide units based on amino acid derivatives, e.g. N-(2-  
 CC aminoethyl)glycine. The nucleic acids are packed into liposomes. The  
 CC products of the invention have antiinflammatory, dermatological,  
 CC antipsoriatic, general endocrine, vulnary and immunosuppressive  
 CC activity and act as interleukin-6 or interleukin-8 release inhibitors.  
 CC The composition is especially useful for preventing or treating  
 CC epithelial inflammations, including inflammation-induced aging,  
 CC psoriasis, atopic eczema, dry skin, alopecia areata, vitiligo, bullous  
 CC diseases, graft versus host reactions, UV-induced skin inflammation and  
 CC parodontosis.

XX SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;  
 Query Match 30.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
 Db 1 RRC 3

## RESULT 84

ID ADL35954/C  
 AC ADL35954 standard; DNA; 6 BP.

XX ADL35954;

XX 20-MAY-2004 (first entry)

XX Non-methylated CpG motif consensus sequence.

XX cosmetic; pharmaceutical; epithelial tissue; fabric softener;  
 KW hand washing product; body care product; hair care product; hair dye;  
 KW manual dishwashing product; nonmethylated CpG; antiinflammatory;  
 KW dermatological; antipsoriatic; endocrine; vulnary; immunosuppressive;  
 KW interleukin-6 release inhibitor; interleukin-8 release inhibitor;  
 KW epithelial inflammation; inflammation-induced aging; psoriasis;  
 KW atopic eczema; dry skin; alopecia areata; vitiligo; bullous disease;  
 KW graft versus host; UV-induced skin inflammation; parodontosis; ds.

XX Unidentified.

XX DE10233994-A1.

XX 12-FEB-2004.

XX 25-JUL-2002; 2002DE-01033994.

XX 25-JUL-2002; 2002DE-01033994.

XX (PHEN-) PHENION GMBH & CO KG.

XX WPI; 2004-192562/19.

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 CC sequence 5'-A/GA/GC/GC/TC/T-3'. The nucleic acids are optionally modified

CC by replacing phosphodiester linkages with methyl phosphonate,  
 CC phosphoramidate, phosphorothioate or hydroxylamine linkages, by replacing  
 CC ribose with other hexo- or pentopyranoses with 3',5'-carbocyclically  
 CC bridged 2'-deoxyribose derivatives or by replacing sugar phosphate units  
 CC with carboxamide units based on amino acid derivatives, e.g. N-(2-  
 CC aminoethyl)glycine. The nucleic acids are packed into liposomes. The  
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 CC antipsoriatic, general endocrine, vulnary and immunosuppressive  
 CC activity and act as interleukin-6 or interleukin-8 release inhibitors.  
 CC The composition is especially useful for preventing or treating  
 CC epithelial inflammations, including inflammation-induced aging,  
 CC psoriasis, atopic eczema, dry skin, alopecia areata, vitiligo, bullous  
 CC diseases, graft versus host reactions, UV-induced skin inflammation and  
 CC parodontosis.

XX SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
 Db 6 RRC 4

## RESULT 85

AAZ88744  
 ID AAZ88744 standard; DNA; 7 BP.

XX AAZ88744;

XX 16-MAY-2000 (first entry)

XX V. cholera VCR element inverse core DNA sequence.

XX Diversity-selected gene; restriction enzyme; adhesin; toxin;  
 KW detoxifying enzyme; VCR element; ss.

XX Vibrio cholerae.

XX WO9964632-A1.

XX 16-DEC-1999.

XX 11-JUN-1999; 99WO-US013295.

XX 12-JUN-1998; 98US-0089086P.

XX 12-JUN-1998; 98US-0089101P.

XX (NEWE ) NEW ENGLAND BIOLABS INC.

XX Raleigh EA, Vaisville R, Morgan RD;

XX WPI; 2000-116558/10.

XX Cloning intact genes used to isolate genes for restriction enzymes.

XX Disclosure; Page 5; 97pp; English.

XX This invention describes a novel method for cloning intact, diversity-  
 CC selected genes (I) from within gene cassettes (GC) which comprises  
 CC identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)  
 CC to these repeats and amplification to produce DNA fragments containing  
 CC (I), ligating these fragments into a vector and transforming cells with  
 CC the vector. This method is used to clone a wide variety of prokaryotic  
 CC genes that provide a selective advantage under particular conditions,  
 CC particularly those that encode restriction enzymes (used as reagents in  
 CC molecular biology); adhesins (for use in coating or for targeting  
 CC molecules or organisms to particular sites, e.g. for competitive  
 CC exclusion of a selected pathogen); detoxifying enzymes; toxins that  
 CC interact with a host, e.g. for synthesis of inhibitors or antagonists of  
 CC the toxin, or in vaccination, or a modification methyltransferase. Intact

CC genes can be cloned directly with a high probability that the orientation  
 CC of expression is known in advance and low probability of association with  
 CC extraneous, possibly toxic, genes. This sequence represents a VCR element  
 CC inverse core DNA sequence isolated from *Vibrio cholera*

XX SQ Sequence 7 BP; 2 A; 1 C; 0 G; 0 T; 0 U; 4 Other;  
 Query Match 30.0%; Score 3; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
 ||||  
 Db 2 YYY 4

RESULT 86  
 AAZ88744/c  
 ID AAZ88744 standard; DNA; 7 BP.

XX AC AAZ88744;  
 XX DT 16-MAY-2000 (first entry)

XX DE V. cholera VCR element inverse core DNA sequence.

XX KW Diversity-selected gene; restriction enzyme; adhesin; toxin;  
 XX KW detoxifying enzyme; VCR element; ss.

XX OS *Vibrio cholerae*.

XX PN WO9964632-A1.  
 XX PD 16-DEC-1999.

XX PF 11-JUN-1999; 99WO-US013295.

XX PR 12-JUN-1998; 98US-0089086P.

XX PR 12-JUN-1998; 98US-0089101P.

XX PA (NEW) NEW ENGLAND BIOLABS INC.  
 XX PI Raleigh EA, Vaisvila R, Morgan RD;

XX DR WPI; 2000-116558/10.

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 CC molecular biology); adhesins (for use in coating or for targeting  
 CC molecules or organisms to particular sites, e.g. for competitive  
 CC exclusion of a selected pathogen); detoxifying enzymes; toxins that  
 CC interact with a host, e.g. for synthesis of inhibitors or antagonists of  
 CC the toxin, or in vaccination, or a modification methyltransferase. Intact  
 CC genes can be cloned directly with a high probability that the orientation  
 CC of expression is known in advance and low probability of association with  
 CC extraneous, possibly toxic, genes. This sequence represents a VCR element  
 CC inverse core DNA sequence isolated from *Vibrio cholera*

XX SQ Sequence 7 BP; 2 A; 1 C; 0 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
 ||||  
 Db 4 RRR 2

RESULT 87  
 AAZ88743  
 ID AAZ88743 standard; DNA; 8 BP.

XX AC AAZ88743;

XX DT 16-MAY-2000 (first entry)

XX DE V. cholera VCR element core DNA sequence.

XX KW Diversity-selected gene; restriction enzyme; adhesin; toxin;  
 XX KW detoxifying enzyme; VCR element; ss.

XX OS *Vibrio cholerae*.

XX PN WO9964632-A1.

XX PD 16-DEC-1999.

XX PF 11-JUN-1999; 99WO-US013295.

XX PR 12-JUN-1998; 98US-0089086P.

XX PR 12-JUN-1998; 98US-0089101P.

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 CC the vector. This method is used to clone a wide variety of prokaryotic  
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 CC particularly those that encode restriction enzymes (used as reagents in  
 CC molecular biology); adhesins (for use in coating or for targeting  
 CC molecules or organisms to particular sites, e.g. for competitive  
 CC exclusion of a selected pathogen); detoxifying enzymes; toxins that  
 CC interact with a host, e.g. for synthesis of inhibitors or antagonists of  
 CC the toxin, or in vaccination, or a modification methyltransferase. Intact  
 CC genes can be cloned directly with a high probability that the orientation  
 CC of expression is known in advance and low probability of association with  
 CC extraneous, possibly toxic, genes. This sequence represents a VCR element  
 CC core DNA sequence isolated from *Vibrio cholera*

XX SQ Sequence 8 BP; 0 A; 0 C; 1 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
 ||||  
 Db 4 RRR 6

RESULT 88  
 AAZ88743/c  
 ID AAZ88743 standard; DNA; 8 BP.

XX

AC AAZ88743;  
 XX 16-MAY-2000 (first entry)  
 DT V. cholera VCR element core DNA sequence.  
 XX Diversity-selected gene; restriction enzyme; adhesin; toxin;  
 DE detoxifying enzyme; VCR element; ss.  
 KW Vibrio cholerae.  
 XX WO9964632-A1.  
 XX 16-DEC-1999.  
 XX 11-JUN-1999; 99WO-US013295.  
 XX 12-JUN-1998; 98US-0089086P.  
 XX 12-JUN-1998; 98US-0089101P.  
 XX (NEW) NEW ENGLAND BIOLABS INC.  
 XX Raleigh EA, Vaisvila R, Morgan RD;  
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 CC to these repeats and amplification to produce DNA fragments containing  
 CC (I), ligating these fragments into a vector and transforming cells with  
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 CC interact with a host, e.g. for synthesis of inhibitors or antagonists of  
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 CC genes can be cloned directly with a high probability that the orientation  
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 CC core DNA sequence isolated from *Vibrio cholera*  
 XX  
 SQ Sequence 8 BP; 0 A; 0 C; 1 G; 2 T; 0 U; 5 Other;  
 Query Match 30.0%; Score 3; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 DB 7 YYY 5  
 RESULT 89  
 AAA28439  
 ID AAA28439 standard; DNA; 8 BP.  
 XX AAA28439;  
 AC 29-AUG-2000 (first entry)  
 DT Synthetic promoter conserved domain IIA.  
 XX Artificial promoter; strong; weak; transgene expression; plant; ss.  
 XX Synthetic.

PN EP1002869-A1.  
 XX 24-MAY-2000.  
 XX 25-FEB-1999; 99EP-00301419.  
 XX 09-NOV-1998; 98IN-DE003322.  
 XX (COUL) CSIR COUNCIL SCI IND RES.  
 XX Tuli R, Sawant SV, Singh PK, Gupta SK;  
 XX WPI; 2000-341712/30.  
 DR New chemically synthesized artificial promoter, useful high level  
 PT expression of transgenes in different organisms.  
 XX Claim 6; Page 17; 40pp; English.  
 XX A chemically synthesized promoter can comprise a conserved domain IIA as  
 CC shown here for high level expression of genes. The sequence comprises a  
 CC tandem repeat of 2-8 nucleotides comprising A/G nucleotides. These  
 CC elements are present beyond position -200 of the promoter. Chemically  
 CC synthesized artificial promoters are new and comprise a DNA sequence  
 CC designed for a targeted level and pattern of gene expression by  
 CC strategically putting together several signature sequences identified by  
 CC sequence alignment and statistical analysis of a large database  
 CC constructed for this purpose. A method for chemically synthesizing an  
 CC artificial promoter for expressing genes at a desired level in different  
 CC organisms is also claimed. The high level expression in a plant using  
 CC such an artificial promoter (e.g. AAA28449) can be measured comprising  
 CC polyethylene glycol (PEG) mediated transformation of plant protoplasts as  
 CC well as biolistic mediated transformation of plant tissues including  
 CC root, stem, intact leaf tissue followed by transient GUS assay to compare  
 CC with a natural CaMV 35S promoter showing the desired level of activity.  
 CC The promoter is useful for high level expression of transgenes in  
 CC different organisms and for testing high level gene expression in plants  
 CC (claimed). The promoter is biologically active and is efficient and can  
 CC be synthesized to express in even the most complex organisms  
 XX  
 SQ Sequence 8 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 8 Other;  
 Query Match 30.0%; Score 3; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRR 3  
 DB 1 RRR 3  
 RESULT 90  
 AAA28439/c  
 ID AAA28439 standard; DNA; 8 BP.  
 XX AAA28439;  
 AC 29-AUG-2000 (first entry)  
 DT Synthetic promoter conserved domain IIA.  
 XX Artificial promoter; strong; weak; transgene expression; plant; ss.  
 XX Synthetic.  
 XX EP1002869-A1.  
 XX 24-MAY-2000.  
 XX 25-FEB-1999; 99EP-00301419.  
 XX 09-NOV-1998; 98IN-DE003322.  
 XX



PA (COUL ) CSIR COUNCIL SCI IND RES.  
 XX Tuli R, Sawant SV, Singh PK, Gupta SK;  
 XX WPI; 2000-341712/30.  
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 CC designed for a targeted level and pattern of gene expression by  
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 CC sequence alignment and statistical analysis of a large database  
 CC constructed for this purpose. A method for chemically synthesizing an  
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 CC organisms is also claimed. The high level expression in a plant using  
 CC such an artificial promoter (e.g. AA28449) can be measured comprising  
 CC polyethylene glycol (PEG) mediated transformation of plant protoplasts as  
 CC well as biolistic mediated transformation of plant tissues including  
 CC root, stem, intact leaf tissue followed by transient GUS assay to compare  
 CC with a natural CamV 35S promoter showing the desired level of activity.  
 CC The promoter is useful for high level expression of transgenes in  
 CC different organisms and for testing high level gene expression in plants  
 CC (claimed). The promoter is biologically active and is efficient and can  
 CC be synthesized to express in even the most complex organisms  
 XX Sequence 8 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 8 Other;  
 SQ Query Match 30.0%; Score 3; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 Db |||  
 8 YYY 6  
 RESULT 91  
 ID AAQ63868 standard; DNA; 9 BP.  
 XX AC AAQ63868;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 10-NOV-1994 (first entry)  
 XX DE Haematopoietic cell factor binding motif from human R gene 5'-UTR.  
 XX KW Immunoglobulin; IgG receptor; gamma-interferon activation; g-IFN;  
 KW haematopoietic cell; protein factor; binding site; GRR motif;  
 KW human high affinity Fc receptor for IgG; human Fc gamma R1; R gene;  
 KW DNA response element; WATE motif; GIRE motif; gene therapy; ds.  
 XX OS Homo sapiens.  
 XX PN FR2696181-A1.  
 XX PD 01-APR-1994.  
 XX PF 25-MAR-2003 (revised)  
 XX DT 10-NOV-1994 (first entry)  
 XX DE Haematopoietic cell factor binding motif from human R gene 5'-UTR.  
 XX KW Immunoglobulin; IgG receptor; gamma-interferon activation; g-IFN;  
 KW haematopoietic cell; protein factor; binding site; GRR motif;  
 KW human high affinity Fc receptor for IgG; human Fc gamma R1; R gene;  
 KW DNA response element; WATE motif; GIRE motif; gene therapy; ds.  
 XX OS Homo sapiens.  
 XX PN FR2696181-A1.  
 XX PD 01-APR-1994.  
 XX PF 25-SEP-1992; 92FR-00011498.  
 XX PR 25-SEP-1992; 92FR-00011498.  
 XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX PI Benech P, Perez C, Wietzerbin J;  
 XX WPI; 1994-128281/16.  
 XX New nucleotide sequences are specific target for proteins exclusive to  
 PT haematopoietic cells - used to impart, to partic. cells, a response to  
 PT gamma-interferon, e.g. for gene therapy.  
 XX Claim 3; Page 25; 37pp; French.  
 XX The region immediately upstream of the sequence which codes for the human  
 CC high affinity Fc receptor for IgG (the R gene) contains binding sites  
 CC specific for haematopoietic cells, including the response element  
 CC sequence AAQ63868. One or more copies of this sequence is preferred for  
 CC conferring on a gene a transcriptional activity limited to haematopoietic  
 CC cells. The DNA motif thus has potential in gene therapy. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX Sequence 9 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 4 Other;  
 SQ Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 Db |||  
 1 YYY 3  
 RESULT 92  
 ID AAQ63868 standard; DNA; 9 BP.  
 XX AC AAQ63868;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 10-NOV-1994 (first entry)  
 XX DE Haematopoietic cell factor binding motif from human R gene 5'-UTR.  
 XX KW Immunoglobulin; IgG receptor; gamma-interferon activation; g-IFN;  
 KW haematopoietic cell; protein factor; binding site; GRR motif;  
 KW human high affinity Fc receptor for IgG; human Fc gamma R1; R gene;  
 KW DNA response element; WATE motif; GIRE motif; gene therapy; ds.  
 XX OS Homo sapiens.  
 XX PN FR2696181-A1.  
 XX PD 01-APR-1994.  
 XX PF 25-SEP-1992; 92FR-00011498.  
 XX PR 25-SEP-1992; 92FR-00011498.  
 XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX PI Benech P, Perez C, Wietzerbin J;  
 XX WPI; 1994-128281/16.  
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 PT haematopoietic cells - used to impart, to partic. cells, a response to  
 PT gamma-interferon, e.g. for gene therapy.  
 XX Claim 3; Page 25; 37pp; French.  
 XX The region immediately upstream of the sequence which codes for the human  
 CC high affinity Fc receptor for IgG (the R gene) contains binding sites  
 CC specific for haematopoietic cells, including the response element  
 CC sequence AAQ63868. One or more copies of this sequence is preferred for  
 CC conferring on a gene a transcriptional activity limited to haematopoietic  
 CC cells. The DNA motif thus has potential in gene therapy. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX

```

SQ Sequence 9 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 4 Other;
  Query Match      30.0%; Score 3; DB 2; Length 9;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 3 RRR 1

RESULT 93
AAT96075
ID AAT96075 standard; DNA; 9 BP.
XX
AC AAT96075;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 15-16; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 9 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 5 Other;
  Query Match      30.0%; Score 3; DB 2; Length 9;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 8 YYY 6

RESULT 95
AAQ31609
ID AAQ31609 standard; DNA; 10 BP.
XX
AC AAQ31609;
XX
DT 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
DE Cauliflower mosaic virus 35S enhancer sequence.
XX

```

KW CaMV; transcription initiation rate; enhancement; variation; ss.  
 XX Cauliflower mosaic virus.  
 OS US5164316-A.  
 XX 17-NOV-1992.  
 XX 17-AUG-1989; 89US-00395155.  
 XX 13-JAN-1987; 87US-00002780.  
 PR 25-JAN-1988; 88US-00147887.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX Mcpherson JC, Kay R;  
 XX WPI; 1992-407146/49.  
 XX New plant cell comprising DNA contg. duplicated cauliflower mosaic virus 35 S enhancer sequence - used to provide enhanced transcription initiation rate.  
 PT Disclosure; Page 7; 12pp; English.  
 XX The sequence is that of a cauliflower mosaic virus 35S enhancer sequence which can be used in a DNA construct which permits variation in enhancement of the transcription initiation rate in the plant cell. This allows the prodn. of new characteristics in transformed plants, e.g. increased prodn. of proteins for agronomical or commercial purposes when the construct contains a protein-coding sequence, or the regulation of exogenous gene expression by competing levels of antisense RNA. (Updated on 25-MAR-2003 to correct PR field.)  
 CC Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;  
 XX Query Match 30.0%; Score 3; DB 2; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX Qy 5 WNG 7  
 XX Db 8 WNG 10  
 XX RESULT 96  
 XX AAQ31609/c  
 XX ID AAQ31609 standard; DNA; 10 BP.  
 XX AC AAQ31609;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 02-APR-1993 (first entry)  
 XX DE Cauliflower mosaic virus 35S enhancer sequence.  
 XX CaMV; transcription initiation rate; enhancement; variation; ss.  
 XX Cauliflower mosaic virus.  
 OS US5164316-A.  
 XX 17-NOV-1992.  
 XX 17-AUG-1989; 89US-00395155.  
 XX 13-JAN-1987; 87US-00002780.  
 PR 25-JAN-1988; 88US-00147887.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX Mcpherson JC, Kay R;  
 XX WPI; 1992-407146/49.  
 XX New plant cell comprising DNA contg. duplicated cauliflower mosaic virus 35 S enhancer sequence - used to provide enhanced transcription initiation rate.  
 PT Disclosure; Page 7; 12pp; English.  
 XX The sequence is that of a cauliflower mosaic virus 35S enhancer sequence which can be used in a DNA construct which permits variation in enhancement of the transcription initiation rate in the plant cell. This allows the prodn. of new characteristics in transformed plants, e.g. increased prodn. of proteins for agronomical or commercial purposes when the construct contains a protein-coding sequence, or the regulation of exogenous gene expression by competing levels of antisense RNA. (Updated on 25-MAR-2003 to correct PR field.)  
 CC Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;  
 XX Query Match 30.0%; Score 3; DB 2; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX Qy 5 WNG 7  
 XX Db 8 WNG 10  
 XX RESULT 97  
 XX AAQ30505  
 XX ID AAQ30505 standard; DNA; 10 BP.  
 XX AC AAQ30505;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 19-MAR-1993 (first entry)  
 XX DE Serum response element under control of TCRE.  
 XX KW Transcriptional control recognition element; decoy; cellular RNA; promoter; hormone receptor element; viral; liver; tissue; viral; proliferation; linker; NF-1; ss.  
 XX OS Synthetic.  
 XX PN WO9218522-A1.  
 XX DT 29-OCT-1992.  
 XX PF 17-APR-1992; 92WO-US003205.  
 XX PR 18-APR-1991; 91US-00687337.  
 XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX PI Chu BC, Orgel L;  
 XX WPI; 1992-382035/46.  
 XX New oligo-nucleotide(s) contg. transcription control recognition element - stabilised by covalent bonding of two DNA strands, act as decoys for regulatory protein to modulate specific RNA.  
 XX Disclosure; Page 6; 41pp; English.  
 XX Transcriptional control recognition element recognition sequences may be recognised by control proteins and are involved in either enhancing or repressing transcription of associated sequences. TCR sequences include promoter elements, hormone receptor elements, viral, cellular, liver or tissue elements, etc. The sequence represents an exemplary general element, the serum response element. A typical application of the TCR element, recognising oligonucleotides is inhibition of viral proliferation. See also AAQ30472-518. (Updated on 25-MAR-2003 to correct PN field.)

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XX SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6
Db 2 CW 4

RESULT 98
AAQ30505/c
ID AAQ30505 standard; DNA; 10 BP.
XX AC AAQ30505;
XX XX
DT 25-MAR-2003 (revised)
DT 19-MAR-1993 (first entry)
XX XX
DE Serum response element under control of TCRE.
XX XX
KW Transcriptional control recognition element; decoy; cellular RNA;
KW promoter; hormone receptor element; viral; liver; tissue; viral;
KW proliferation; linker; NF-1; ss.
XX XX
OS Synthetic.
XX XX
PN WO9218522-A1.
XX XX
PD 29-OCT-1992.
XX XX
PF 17-APR-1992; 92WO-US003205.
XX XX
PR 18-APR-1991; 91US-00687337.
XX XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX XX
PI Chu BC, Orgel L;
XX XX
DR WPI; 1992-382035/46.
XX XX
PT New oligo-nucleotide(s) contg. transcription control recognition element
PT - stabilised by covalent bonding of two DNA strands, act as decoys for
PT regulatory protein to modulate specific RNA.
XX PS
XX Disclosure; Page 6; 41pp; English.
XX CC
XX Transcriptional control recognition element recognition sequences may be
XX recognised by control proteins and are involved in either enhancing or
XX repressing transcription of associated sequences. TCR sequences include
XX promoter elements, hormone receptor elements, viral, cellular, liver or
XX tissue elements, etc. The sequence represents an exemplary general
XX element, the serum response element. A typical application of the TCRE
XX recognising oligonucleotides is inhibition of viral proliferation. See
XX also AAQ30472-518. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6
Db 9 CW 7

RESULT 99
AAQ38817
ID AAQ38817 standard; DNA; 10 BP.
XX AC AAQ38817;
XX XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1993 (first entry)
XX XX
DE CaMV 35S promoter repeat unit.
XX XX
KW Cauliflower mosaic virus; enhancer; construct; ss.
XX OS Synthetic.
XX XX
PN US5196525-A.
XX XX
PD 23-MAR-1993.
XX XX

AAQ38817;
25-MAR-2003 (revised)
27-JUL-1993 (first entry)
CaMV 35S promoter repeat unit.
Cauliflower mosaic virus; enhancer; construct; ss.
Synthetic.
US5196525-A.
23-MAR-1993.
08-APR-1991; 91US-00682049.
13-JAN-1987; 87US-00002780.
25-JAN-1988; 88US-00147887.
17-AUG-1989; 89US-00395155.
(UYBR-) UNIV BRITISH COLUMBIA.
Mcpherson JC, Kay R;
WPI; 1993-116860/14.
DNA construct for varying transcription initiation rate enhancement in
plants - comprises transcription initiation region with tandem duplicated
cauliflower mosaic virus 35-S enhancer sequence, nucleotide sequence, and
termination region.
Disclosure; Page 7; 12pp; English.
The sequence represents a single repeat unit of the CaMV 35S promoter.
Synthetic enhancer domains comprise a plurality of the units of the
natural enhancer spaced in the same was as in the natural enhancer. The
synthetic enhancer domains may be used in DNA constructs which allow for
increased rate of transcription. These constructs have wide application
in the control of the formation of expression prods. and protection
against pathogens or antibiotics, etc. See also AAQ38816. (Updated on 25-
MAR-2003 to correct PF field.)
XX SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
Db 8 WWG 10

RESULT 100
AAQ38817/c
ID AAQ38817 standard; DNA; 10 BP.
XX AC AAQ38817;
XX XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1993 (first entry)
XX XX
DE CaMV 35S promoter repeat unit.
XX XX
KW Cauliflower mosaic virus; enhancer; construct; ss.
XX OS Synthetic.
XX XX
PN US5196525-A.
XX XX
PD 23-MAR-1993.
XX XX

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PF 08-APR-1991; 91US-00682049.
XX
XX
PR 13-JAN-1987; 87US-00002780.
PR 25-JAN-1988; 88US-00147887.
PR 17-AUG-1989; 89US-00395155.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Mcpherson JC, Kay R;
XX
XX WPI; 1993-116860/14.
XX
XX DNA construct for varying transcription initiation rate enhancement in
PT plants - comprises transcription initiation region with tandem duplicated
PT cauliflower mosaic virus 35-S enhancer sequence, nucleotide sequence, and
PT termination region.
XX
XX Disclosure; Page 7; 12pp; English.
XX
XX The sequence represents a single repeat unit of the CaMV 35S promoter.
XX Synthetic enhancer domains comprise a plurality of the units of the
XX natural enhancer spaced in the same was as in the natural enhancer. The
XX synthetic enhancer domains may be used in DNA constructs which allow for
XX increased rate of transcription. These constructs have wide application
XX in the control of the formation of expression prods. and protection
XX against pathogens or antibiotics, etc. See also AAQ38816. (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;
SQ
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 5
DB 10 CWV 8

RESULT 101
AAQ72970
ID AAQ72970 standard; DNA; 10 BP.
XX
XX AC AAQ72970;
XX
XX DT 25-MAR-2003 (revised)
XX 30-JUN-1995 (first entry)
XX
XX Engineered enhancer element repeat unit in CaMV35S promoter.
XX
XX Enhancer element; repeat unit; promoter; cauliflower mosaic virus;
XX CaMV35S; enhancer region; core sequence; variability; transgenic; plant;
XX expression; foreign gene; pathogen; antibiotic; ss.
XX
XX Synthetic.
XX
XX OS US5359142-A.
XX
XX PN 25-OCT-1994.
XX
XX PD 09-MAR-1994; 94US-00209752.
XX
XX PF 13-JAN-1987; 87US-00002780.
XX 25-JAN-1988; 88US-00147887.
XX 17-AUG-1989; 89US-00395155.
XX 17-NOV-1992; 92US-00977600.
XX
XX (MONS ) MONSANTO CO.
XX
XX PA Kay R, Mcpherson JC;
XX
XX PI WPI; 1994-341080/42.
XX
XX Novel differentiated plants contg improved DNA constructs - with
XX engineered enhancer element to enhance expression of foreign genes.
XX Disclosure; Col 3; 11pp; English.

PT Novel differentiated plants contg improved DNA constructs - with
PT engineered enhancer element to enhance expression of foreign genes.
XX
XX Disclosure; Col 3; 11pp; English.
XX
XX The sequence of a modified enhancer sequence used to construct a
XX heterologous enhancer/promoter region for the improved expression of
XX genes under control of the modified enhancer promoter in plants. The
XX engineered enhancer region may contain portions of the sequence shown, at
XX least the sequence GTGG or its complementary sequence. The promoter may
XX the 35S promoter of the cauliflower mosaic virus (CaMV35S) or a
XX heterologous promoter e.g. the T DNA gene 5 or 7 promoter. The engineered
XX enhancer/promoter preferably has an enhancer domain with one more repeat
XX than the 35S enhancer. The natural enhancer sequence can be repeated
XX several times in the enhancer region. The repeats can comprise of 4-16
XX bases, generally 4, 7, or 10 base repeats. The repeat structure may be
XX imperfect, containing a core sequence surrounded by regions of
XX variability. Transgenic plants show increased expression of foreign genes
XX due to the presence of the engineered enhancer sequences. The improved
XX constructions have wide applications e.g. in the control of the formation
XX of products, protection against pathogens or antibiotics. (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;
SQ
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WVG 7
DB 8 WVG 10

RESULT 102
AAQ72970/c
ID AAQ72970 standard; DNA; 10 BP.
XX
XX AC AAQ72970;
XX
XX DT 25-MAR-2003 (revised)
XX 30-JUN-1995 (first entry)
XX
XX Engineered enhancer element repeat unit in CaMV35S promoter.
XX
XX Enhancer element; repeat unit; promoter; cauliflower mosaic virus;
XX CaMV35S; enhancer region; core sequence; variability; transgenic; plant;
XX expression; foreign gene; pathogen; antibiotic; ss.
XX
XX Synthetic.
XX
XX OS US5359142-A.
XX
XX PN 25-OCT-1994.
XX
XX PD 09-MAR-1994; 94US-00209752.
XX
XX PF 13-JAN-1987; 87US-00002780.
XX 25-JAN-1988; 88US-00147887.
XX 17-AUG-1989; 89US-00395155.
XX 17-NOV-1992; 92US-00977600.
XX
XX (MONS ) MONSANTO CO.
XX
XX PA Kay R, Mcpherson JC;
XX
XX PI WPI; 1994-341080/42.
XX
XX Novel differentiated plants contg improved DNA constructs - with
XX engineered enhancer element to enhance expression of foreign genes.
XX Disclosure; Col 3; 11pp; English.
XX

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CC The sequence of a modified enhancer sequence used to construct a  
 CC heterologous enhancer/promoter region for the improved expression of  
 CC genes under control of the modified enhancer promoter in plants. The  
 CC engineered enhancer region may contain portions of the sequence shown, at  
 CC least the sequence GTGG or its complementary sequence. The promoter may  
 CC the 35S promoter of the cauliflower mosaic virus (CaMV35S) or a  
 CC heterologous promoter e.g. the T DNA gene 5 or 7 promoter. The engineered  
 CC enhancer/promoter preferably has an enhancer domain with one more repeat  
 CC than the 35S enhancer. The natural enhancer sequence can be repeated  
 CC several times in the enhancer region. The repeats can comprise of 4-16  
 CC bases, generally 4, 7, or 10 base repeats. The repeat structure may be  
 CC imperfect, containing a core sequence surrounded by regions of  
 CC variability. Transgenic plants show increased expression of foreign genes  
 CC due to the presence of the engineered enhancer sequences. The improved  
 CC constructions have wide applications e.g. in the control of the formation  
 CC of products, protection against pathogens or antibiotics. (Updated on 25-  
 CC MAR-2003 to correct PF field.)

SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6  
 DB 10 CWV 8

## RESULT 103

AAQ81756  
 ID AAQ81756 standard; DNA; 10 BP.

AC AAQ81756;

XX 25-MAR-2003 (revised)

DT 27-FEB-1995 (first entry)

DE CaMV 35S enhancer repetitive unit.

XX CaMV; enhancer; promoter; repetitive unit; transcription; initiation; ss.

XX Cauliflower mosaic virus.

XX US5322938-A.

XX 21-JUN-1994.

XX 17-NOV-1992; 92US-00977600.

XX 13-JAN-1987; 87US-00002780.

XX 25-JAN-1988; 88US-00147887.

XX 17-AUG-1989; 89US-00395155.

XX (MONS ) MONSANTO CO.

XX Mcpherson JC, Kay R;

XX WPI; 1994-199579/24.

XX Transcription initiation regions with enhanced transcription efficiency -  
 XX comprise tandemly duplicated CaMV 35S enhancer sequences and a promoter.

XX Disclosure; Col 3; 12pp; English.

XX Many viral, plant and animal enhancers contain sets of repeated sequence  
 XX elements, such as the sequences given in AAQ81755-56. These units are  
 XX repeated several times within the upstream sequence of the CaMV 35S  
 XX promoter region. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7  
 DB 8 WWG 10

## RESULT 104

AAQ81756/c  
 ID AAQ81756 standard; DNA; 10 BP.

XX AC AAQ81756;

XX 25-MAR-2003 (revised)

DT 27-FEB-1995 (first entry)

XX CaMV 35S enhancer repetitive unit.

XX CaMV; enhancer; promoter; repetitive unit; transcription; initiation; ss.

XX Cauliflower mosaic virus.

XX US5322938-A.

XX 21-JUN-1994.

XX 17-NOV-1992; 92US-00977600.

XX 13-JAN-1987; 87US-00002780.

XX 25-JAN-1988; 88US-00147887.

XX 17-AUG-1989; 89US-00395155.

XX (MONS ) MONSANTO CO.

XX Mcpherson JC, Kay R;

XX WPI; 1994-199579/24.

XX Transcription initiation regions with enhanced transcription efficiency -  
 XX comprise tandemly duplicated CaMV 35S enhancer sequences and a promoter.

XX Disclosure; Col 3; 12pp; English.

XX Many viral, plant and animal enhancers contain sets of repeated sequence  
 XX elements, such as the sequences given in AAQ81755-56. These units are  
 XX repeated several times within the upstream sequence of the CaMV 35S  
 XX promoter region. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6  
 DB 10 CWV 8

## RESULT 105

AAAT96065  
 ID AAAT96065 standard; DNA; 10 BP.

XX AC AAAT96065;

XX 31-MAR-1998 (first entry)

XX Recombination region homologous to SINE flanking region.

XX Recombination region; consensus defined flanking region;

XX short interspersed repeated DNA element; SINE; ss.

```

OS Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX 07-MAY-1996; 96US-00643886.
XX 31-AUG-1995; 95US-0003063P.
XX (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 1; Col 11-12; 12pp; English.
XX Integrating a DNA sequence into the genome of a vertebrate host cell,
XX comprises introducing a construct comprising the DNA sequence and a
XX recombination region homologous to a consensus defined flanking region of
XX a short interspersed repeated DNA element (SINE), e.g. the present
XX sequence. The method may be used to modify the phenotype of cells, or
XX investigate the response of receptors, metabolic pathways or expression
XX products involved in the regulation of transcription or transduction of
XX signals. It may also be used to produce protein products and transgenic
XX animals, by providing novel capabilities to the cells or inhibiting
XX endogenous capabilities, investigate physiological indications and screen
XX cosmetics, foods and drugs. By using antisense sequences effective
XX inhibition of both copies of a gene is possible, ensuring the substantial
XX absence of the particular transcriptional or translational product. In
XX addition the method may enhance efficiency in gene therapy, when
XX providing for a capability in which the host is deficient
XX Sequence 10 BP; 3 A; 0 C; 0 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
DB 7 YYY 9

RESULT 106
AAT96065/C
ID AAT96065 standard; DNA; 10 BP.
XX AAT96065;
XX 31-MAR-1998 (first entry)
XX Recombination region homologous to SINE flanking region.
XX Recombination region; consensus defined flanking region;
XX short interspersed repeated DNA element; SINE; ss.
XX Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX Recombination region homologous to SINE flanking region.
XX Recombination region; consensus defined flanking region;
XX short interspersed repeated DNA element; SINE; ss.
XX Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX 07-MAY-1996; 96US-00643886.
XX 31-AUG-1995; 95US-0003063P.
XX (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 7; Col 15-16; 12pp; English.

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XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 1; Col 11-12; 12pp; English.
XX Integrating a DNA sequence into the genome of a vertebrate host cell,
XX comprises introducing a construct comprising the DNA sequence and a
XX recombination region homologous to a consensus defined flanking region of
XX a short interspersed repeated DNA element (SINE), e.g. the present
XX sequence. The method may be used to modify the phenotype of cells, or
XX investigate the response of receptors, metabolic pathways or expression
XX products involved in the regulation of transcription or transduction of
XX signals. It may also be used to produce protein products and transgenic
XX animals, by providing novel capabilities to the cells or inhibiting
XX endogenous capabilities, investigate physiological indications and screen
XX cosmetics, foods and drugs. By using antisense sequences effective
XX inhibition of both copies of a gene is possible, ensuring the substantial
XX absence of the particular transcriptional or translational product. In
XX addition the method may enhance efficiency in gene therapy, when
XX providing for a capability in which the host is deficient
XX Sequence 10 BP; 3 A; 0 C; 0 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
DB 9 RRR 7

RESULT 107
AAT96076
ID AAT96076 standard; DNA; 10 BP.
XX AAT96076;
XX 31-MAR-1998 (first entry)
XX Recombination region homologous to SINE flanking region.
XX Recombination region; consensus defined flanking region;
XX short interspersed repeated DNA element; SINE; ss.
XX Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX 07-MAY-1996; 96US-00643886.
XX 31-AUG-1995; 95US-0003063P.
XX (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 7; Col 15-16; 12pp; English.

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CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC animals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient

XX Sequence 10 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

DB 7 RRR 9

#### RESULT 108

AAT96076/c  
 ID AAT96076 standard; DNA; 10 BP.

AC AAT96076;

XX 31-MAR-1998 (first entry)

XX Recombination region homologous to SINE flanking region.

XX Recombination region; consensus defined flanking region;  
 KW short interspersed repeated DNA element; SINE; ss.

XX Synthetic.

XX US5695977-A.

XX 09-DEC-1997.

XX 07-MAY-1996; 96US-00643886.

XX 31-AUG-1995; 95US-0003063P.

XX (GENE-) GENETIC INFORMATION RES INST.

XX Jurka JW;

XX WPI; 1998-041303/04.

XX Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.

XX Claim 7; Col 15-16; 12pp; English.

XX Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC animals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective

CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient

XX Sequence 10 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

DB 9 YYY 7

#### RESULT 109

AAX88060

ID AAX88060 standard; cDNA; 10 BP.

AC AAX88060;

XX 08-SEP-1999 (first entry)

XX Serum response factor inner core DNA.

XX Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;  
 KW RNA stability element; gene therapy; muscle atrophy; neurological;  
 KW muscular disease; systemic disease; aging; trophic factor; haemophilia;  
 KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;  
 KW cerebrovascular; peripheral-vascular disease; hormone deficiency;  
 KW diabetes; transgenic animal; carcinogen; regulatory element;  
 KW livestock improvement; immune response; ss.

XX Unidentified.

XX US5925564-A.

XX 20-JUL-1999.

XX 07-JUN-1995; 95US-00472809.

XX 06-NOV-1991; 91US-00789919.

XX 09-MAR-1994; 94US-00209846.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX O'malley BW, Demayo FJ, Schwartz RJ;

XX WPI; 1999-418276/35.

XX New expression vector system useful for gene therapy.

XX Disclosure; Col 39-40; 67pp; English.

XX This invention describes novel expression vector systems containing RNA  
 CC stability elements from 3' flanking sequences used for establishing  
 CC expression of a nucleic acid sequence within a tissue. The vectors also  
 CC facilitate enhanced expression in tissues and target expression with  
 CC tissue specificity. The expression vectors can be used to treat diseases  
 CC through gene therapy by targeting the vector to specific tissues.  
 CC Diseases that can be treated include muscle atrophy associated with  
 CC neurological, muscular or systemic disease, aging by causing tissues to  
 CC express trophic factors, haemophilia by causing tissues to express and  
 CC secrete clotting factor into the circulation, atherogenesis and  
 CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular  
 CC disease by causing tissues to express factors involved in tissue  
 CC metabolism. They can be used to replace genes of inherited genetic  
 CC defects or acquired hormone deficiencies e.g. diabetes. To transform  
 CC cells to produce particular proteins or RNA in vitro. To create  
 CC transgenic animals which can be used for research into human diseases,  
 CC assessing novel therapeutic methods, assessing the effect of chemical and  
 CC physical carcinogens and for studying the effect of genes and genetic



CC regulatory elements or livestock improvement. They can be used to induce  
 CC an immune response. These vectors provide controlled expression of the  
 CC genes they carry and produce a significantly high level of expression.  
 CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the  
 CC vectors which causes increased expression

SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
 |||  
 Db 2 CWW 4

RESULT 110  
 AAX88060/C  
 ID AAX88060 standard; cDNA; 10 BP.

XX AAX88060;

XX 08-SEP-1999 (first entry)

XX Serum response factor inner core DNA.

XX Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;  
 KW RNA stability element; gene therapy; muscle atrophy; neurological;  
 KW muscular disease; systemic disease; aging; trophic factor; haemophilia;  
 KW clotting factor; atherosclerosis; atherosclerotic; cardiovascular;  
 KW cerebrovascular; peripheral-vascular disease; hormone deficiency;  
 KW diabetes; transgenic animal; carcinogen; regulatory element;  
 KW livestock improvement; immune response; ss.

XX Unidentified.

OS

XX US5925564-A.

XX 20-JUL-1999.

XX 07-JUN-1995; 95US-00472809.

XX 06-NOV-1991; 91US-00789919.

XX 09-MAR-1994; 94US-00209846.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX O'malley BW, Demayo FU, Schwartz RJ;

XX WPI; 1999-418276/35.

XX New expression vector system useful for gene therapy.

XX Disclosure; Col 39-40; 67pp; English.

CC This invention describes novel expression vector systems containing RNA  
 CC stability elements from 3' flanking sequences used for establishing  
 CC expression of a nucleic acid sequence within a tissue. The vectors also  
 CC facilitate enhanced expression in tissues and target expression with  
 CC tissue specificity. The expression vectors can be used to treat diseases  
 CC through gene therapy by targeting the vector to specific tissues.  
 CC Diseases that can be treated include muscle atrophy associated with  
 CC neurological, muscular or systemic disease, aging by causing tissues to  
 CC express trophic factors, haemophilia by causing tissues to express and  
 CC secrete clotting factor into the circulation, atherosclerosis and  
 CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular  
 CC disease by causing tissues to express factors involved in tissue  
 CC metabolism. They can be used to replace genes of inherited genetic  
 CC defects or acquired hormone deficiencies e.g. diabetes. To transform  
 CC cells to produce particular proteins or RNA in vitro. To create  
 CC transgenic animals which can be used for research into human diseases,  
 CC assessing novel therapeutic methods, assessing the effect of chemical and

CC physical carcinogens and for studying the effect of genes and genetic  
 CC regulatory elements or livestock improvement. They can be used to induce  
 CC an immune response. These vectors provide controlled expression of the  
 CC genes they carry and produce a significantly high level of expression.  
 CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the  
 CC vectors which causes increased expression

SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
 |||  
 Db 9 CWW 7

RESULT 111

AAA91882

ID AAA91882 standard; DNA; 10 BP.

XX AAA91882;

XX 08-JAN-2001 (first entry)

XX Complement of SNP site beginning at position 546 of the TGFb-RII gene.

XX TGFb-RII; promoter; gene therapy; end-stage renal disease; ESRD;

XX single nucleotide polymorphism; SNP; human; primer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX variation replace(7,T)

XX /\*tag= a

XX WO200049169-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-US004251.

XX 19-FEB-1999; 99US-0120787P.

XX (DZGE-) DZGENES LLC.

XX Moskowicz DW;

XX WPI; 2000-549279/50.

XX Diagnosing genetic susceptibility for end-stage renal disease using  
 XX single nucleotide polymorphisms, involves analyzing sample obtained from  
 XX subject to detect genetic polymorphism in the sample polynucleotide.

XX Example 4; Page 38; 73pp; English.

XX The present invention relates the diagnosis of genetic susceptibility for  
 XX end-stage renal disease (ESRD). The method involves analysing a  
 XX polynucleotide sample for a single nucleotide polymorphism (SNP)  
 XX associated with an altered susceptibility for ESRD. The method allows  
 XX early detection of ESRD and hence effective delay or ideally, prevention  
 XX of ESRD is made possible. The present sequence is a SNP site found in the  
 XX human TGFb-RII promoter sequence (see AAA91882). Polymorphisms in this  
 XX gene are known to be a probable trigger for renal apoptosis

SQ Sequence 10 BP; 0 A; 3 C; 1 G; 1 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCW 5  
 Db |||  
 2 RCW 4

RESULT 112  
 AAA91882/c  
 ID AAA91882 standard; DNA; 10 BP.  
 AC  
 XX  
 AC AAA91882;  
 XX  
 DT 08-JAN-2001 (first entry)  
 XX  
 DE Complement of SNP site beginning at position 546 of the TGFb-RII gene.  
 XX  
 KW TGFb-RII; promoter; gene therapy; end-stage renal disease; ESRD;  
 KW single nucleotide polymorphism; SNP; human; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT variation replace(7,T)  
 FT /tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"  
 XX  
 PN WO200049169-A1.  
 XX  
 XX 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004251.  
 XX  
 PR 19-FEB-1999; 99US-0120787P.  
 XX  
 PA (DZGE-) DZGENES LLC.  
 XX  
 XX Moskowitz DW;  
 PI  
 XX WPI; 2000-549279/50.  
 XX  
 DR  
 XX Diagnosing genetic susceptibility for end-stage renal disease using  
 PT single nucleotide polymorphisms, involves analyzing sample obtained from  
 PT subject to detect genetic polymorphism in the sample polynucleotide.  
 XX  
 PS Example 4; Page 38; 73pp; English.  
 XX  
 CC The present invention relates the diagnosis of genetic susceptibility for  
 CC end-stage renal disease (ESRD). The method involves analysing a  
 CC polynucleotide sample for a single nucleotide polymorphism (SNP)  
 CC associated with an altered susceptibility for ESRD. The method allows  
 CC early detection of ESRD and hence effective delay or ideally, prevention  
 CC of ESRD is made possible. The present sequence is a SNP site found in the  
 CC human TGFb-RII promoter sequence (see AAA91867). Polymorphisms in this  
 CC gene are known to be a probable trigger for renal apoptosis  
 XX  
 SQ Sequence 10 BP; 0 A; 3 C; 1 G; 1 T; 0 U; 5 Other;  
 Query Match 30.0%; Score 3; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGY 8  
 Db |||  
 4 WGY 2

RESULT 113  
 AAA16552  
 ID AAA16552 standard; DNA; 10 BP.  
 XX  
 XX  
 AC AAA16552;  
 XX  
 DT 16-JUN-2000 (first entry)  
 XX

DE Initiator consensus sequence SEQ ID NO:23.  
 XX  
 KW Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;  
 KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;  
 KW MN/CA IX isoenzyme; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6027887-A.  
 XX  
 PD 22-FEB-2000.  
 XX  
 PF 24-JAN-1997; 97US-00787739.  
 XX  
 PR 21-OCT-1992; 92US-00964589.  
 PR 30-DEC-1993; 93US-00177093.  
 PR 15-JUN-1994; 94US-00260190.  
 PR 07-JUN-1995; 95US-00477504.  
 PR 07-JUN-1995; 95US-00481658.  
 PR 07-JUN-1995; 95US-00485049.  
 PR 07-JUN-1995; 95US-00485862.  
 PR 07-JUN-1995; 95US-00485863.  
 PR 07-JUN-1995; 95US-00486756.  
 PR 07-JUN-1995; 95US-00487077.  
 XX  
 PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.  
 XX  
 XX Pastorek J, Zavada J, Pastorekova S;  
 FI WPI; 2000-194827/17.  
 XX  
 DR  
 XX Nucleic acid based assay for diagnosing a wide variety of  
 PT preneoplastic/neoplastic disease comprises screening for the presence of  
 PT abnormal MN gene expression in a vertebrate.  
 FT  
 XX  
 PS Disclosure; Col 85; 87pp; English.  
 XX  
 CC The present invention describes a method of screening for  
 CC preneoplastic/neoplastic disease. The method comprises: (1) determining  
 CC whether abnormal MN gene expression is present in a vertebrate; and (2)  
 CC if abnormal MN gene expression is determined to be present in the  
 CC vertebrate, determining that the vertebrate has a significant risk of  
 CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and  
 CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN  
 CC protein is a tumour associated carbonic anhydrase isoenzyme. The method  
 CC is used for detecting a wide variety of preneoplastic/neoplastic diseases  
 CC in a vertebrate, preferably a human. The disease detected is mammary,  
 CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,  
 CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,  
 CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,  
 CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric  
 CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal  
 CC mucosa, pancreatic duct epithelium or liver duct epithelium  
 CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to  
 CC AAY53245 represent sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;  
 Query Match 30.0%; Score 3; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
 Db |||  
 1 YYY 3

RESULT 114  
 AAA16552/c  
 ID AAA16552 standard; DNA; 10 BP.  
 XX  
 XX AAA16552;  
 AC

XX 16-JUN-2000 (first entry)  
XX Initiator consensus sequence SEQ ID NO:23.  
XX Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;  
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;  
KW MN/CA IX isoenzyme; PCR primer; ss.  
XX Homo sapiens.  
XX US6027887-A.  
XX 22-FEB-2000.  
XX 24-JAN-1997; 97US-00787739.  
XX 21-OCT-1992; 92US-00964589.  
XX 30-DEC-1993; 93US-00177093.  
XX 15-JUN-1994; 94US-00260190.  
XX 07-JUN-1995; 95US-00477504.  
XX 07-JUN-1995; 95US-00481658.  
XX 07-JUN-1995; 95US-00485049.  
XX 07-JUN-1995; 95US-00485862.  
XX 07-JUN-1995; 95US-00485863.  
XX 07-JUN-1995; 95US-00486756.  
XX 07-JUN-1995; 95US-00487077.  
XX (SUSC-) SLOVAK ACAD SCI INST VIROLOGY.  
XX Pastorek J, Zavada J, Pastorekova S;  
XX WPI; 2000-194827/17.  
XX Nucleic acid based assay for diagnosing a wide variety of  
PT preneoplastic/neoplastic disease comprises screening for the presence of  
PT abnormal MN gene expression in a vertebrate.  
XX Disclosure; Col 85; 87pp; English.  
XX The present invention describes a method of screening for  
CC preneoplastic/neoplastic disease. The method comprises: (1) determining  
CC whether abnormal MN gene expression is present in a vertebrate; and (2)  
CC if abnormal MN gene expression is determined to be present in the  
CC vertebrate, determining that the vertebrate has a significant risk of  
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and  
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN  
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method  
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases  
CC in a vertebrate, preferably a human. The disease detected is mammary,  
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,  
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,  
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,  
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric  
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal  
CC mucosa, pancreatic duct epithelium or liver duct epithelium  
CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to  
CC AAY53245 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRR 3  
Db 10 RRR 8  
RESULT 115  
AAA52471

AA52471 standard; DNA; 10 BP.  
AA52471;  
25-SEP-2000 (first entry)  
Initiator (Inr) element consensus sequence.  
MN protein; tumour associated cell adhesion molecule; oncoprotein;  
proteoglycan domain; PG domain; carbonic anhydrase; CA domain;  
abnormal expression; neoplastic disease; cancer; gene therapy; promoter;  
consensus initiator element; Inr; ds.  
Unidentified.  
WO200024913-A2.  
04-MAY-2000.  
22-OCT-1999; 99WO-US024879.  
23-OCT-1998; 98US-00177776.  
23-OCT-1998; 98US-00178115.  
(FARB ) BAYER CORP.  
(VIRO-) INST VIROLOGY.  
Zavada J, Pastorekova S, Pastorek J;  
WPI; 2000-350752/30.  
A molecule which specifically binds to a site on MN protein (oncoprotein)  
and prevents adhesion of vertebrate cells to the protein, useful for  
treating preneoplastic or neoplastic diseases such as cancer.  
Disclosure; Page 27; 154pp; English.  
The invention relates to the inhibition of cell adhesion mediated by the  
MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250  
protein). The MN protein is a tumour-associated adhesion molecule which  
comprises a proteoglycan-like (PG) domain (AAB03017) which contains the  
protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).  
Abnormal expression of the MN protein is associated with tumorigenicity.  
The invention encompasses molecules (e.g., proteins and peptides) which  
which specifically bind to a site on the MN protein, thereby preventing  
adhesion of vertebrate cells to the protein in a cell adhesion assay. It  
also encompasses MN proteins or MN protein fragments which can be added  
to the extracellular environment to prevent the adhesion of vertebrate  
cells to each other. The invention also relates to the identification of  
the binding site of the MN protein and to a method of identifying a site  
on an MN protein to which cells adhere, comprising testing a series of  
overlapping peptides from the protein in a cell adhesion assay. The  
invention encompasses a vector comprising an expression control sequence  
operatively linked to a nucleic acid encoding the variable domains of a  
MN-specific antibody, where the domains are separated by a flexible  
linker peptide (AAB03035) and the vector inhibits the growth of a  
vertebrate preneoplastic or neoplastic cell that abnormally expresses MN  
protein. The invention also encompasses a vector comprising a nucleic  
acid encoding a cytotoxic protein or peptide operatively linked to the MN  
gene promoter, which inhibits the growth of a vertebrate preneoplastic or  
neoplastic cell. Also claimed is a repressor complex that binds to the MN  
gene promoter (AA52473). MN proteins and peptides, MN-binding proteins  
and peptides, and expression vectors encoding such proteins and peptides  
are useful for treating patients with preneoplastic or neoplastic disease  
(e.g., cancers) associated with or characterised by abnormal MN  
expression. The present sequence represents a consensus initiator (Inr)  
element  
SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
Db |||  
1 YYY 3

RESULT 116  
AAAS2471/c  
ID AAAS2471 standard; DNA; 10 BP.  
XX  
AC AAAS2471;  
XX  
DT 25-SEP-2000 (first entry)  
XX  
DE Initiator (Inr) element consensus sequence.  
XX  
KW MN protein; tumour associated cell adhesion molecule; oncoprotein;  
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;  
KW abnormal expression; neoplastic disease; cancer; gene therapy; promoter;  
KW consensus initiator element; Inr; ds.  
XX  
OS Unidentified.  
XX  
PN WO200024913-A2.  
XX  
PD 04-MAY-2000.  
XX  
PF 22-OCT-1999; 99WO-US024879.  
XX  
PR 23-OCT-1998; 98US-00177776.  
PR 23-OCT-1998; 98US-00178115.  
XX  
PA (FARB ) BAYER CORP.  
PA (VIRO-) INST VIROLOGY.  
XX  
Zavada J, Pastorekova S, Pastorek J;  
WPI; 2000-350752/30.  
XX  
A molecule which specifically binds to a site on MN protein (oncoprotein)  
PT and prevents adhesion of vertebrate cells to the protein, useful for  
PT treating preneoplastic or neoplastic diseases such as cancer.  
XX  
Disclosure; Page 27; 154pp; English.

The invention relates to the inhibition of cell adhesion mediated by the  
CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250  
CC protein). The MN protein is a tumour-associated adhesion molecule which  
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the  
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).  
CC Abnormal expression of the MN protein is associated with tumorigenicity.  
CC The invention encompasses molecules (e.g., proteins and peptides) which  
CC which specifically bind to a site on the MN protein, thereby preventing  
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It  
CC also encompasses MN proteins or MN protein fragments which can be added  
CC to the extracellular environment to prevent the adhesion of vertebrate  
CC cells to each other. The invention also relates to the identification of  
CC the binding site of the MN protein and to a method of identifying a site  
CC on an MN protein to which cells adhere, comprising testing a series of  
CC overlapping peptides from the protein in a cell adhesion assay. The  
CC invention encompasses a vector comprising an expression control sequence  
CC operatively linked to a nucleic acid encoding the variable domains of a  
CC MN-specific antibody, where the domains are separated by a flexible  
CC linker peptide (AAB03035) and the vector inhibits the growth of a  
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN  
CC protein. The invention also encompasses a vector comprising a nucleic  
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN  
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or  
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN  
CC gene promoter (AAAS2473). MN proteins and peptides, MN-binding proteins  
CC and peptides, and expression vectors encoding such proteins and peptides  
CC are useful for treating patients with preneoplastic or neoplastic disease  
CC (e.g., cancers) associated with or characterised by abnormal MN

CC expression. The present sequence represents a consensus initiator (Inr)  
CC element  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
Db |||  
10 RRR 8

RESULT 117  
AAH26710  
ID AAH26710 standard; DNA; 10 BP.  
XX  
AC AAH26710;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE CARG box motif.  
XX  
KW CARG box; smooth muscle 22 alpha; SM22-alpha; promoter; mouse;  
KW restenosis; atherosclerosis; asthma; cell proliferation; antiasthmatic;  
KW antiarteriosclerotic; gene therapy; ss.  
XX  
OS Mammalia.  
XX  
PN US6284743-B1.  
XX  
PD 04-SEP-2001.  
XX  
PF 10-APR-2000; 2000US-00546550.  
XX  
PR 05-OCT-1995; 95US-0004868P.  
PR 07-OCT-1996; 96US-00728807.  
PR 26-FEB-1999; 99US-00258367.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Parmacek MS, Solway J;  
XX  
WPI; 2001-588977/66.  
XX  
Modulating smooth muscle cell proliferation in a mammal, useful for  
PT treating or preventing proliferation diseases, e.g. atherosclerosis,  
PT restenosis or asthma, comprises contacting cells with smooth muscle 22  
PT alpha gene promoter.  
XX  
Example 9; Col 34; 68pp; English.

The present sequence is that of a CARG box motif. The motif is present in  
CC smooth muscle elements 1 and 4 of the mouse smooth muscle 22 alpha (SM22-  
CC alpha) gene promoter (see AAH26682). CARG boxes are involved in the  
CC binding of the MADS box transcription factor SRP, and may play an  
CC important role in regulating the transcription of genes encoding skeletal  
CC and cardiac alpha-actin. The invention provides methods of preventing  
CC restenosis following balloon angioplasty and methods of treating asthma.  
CC The methods are based on inhibition of smooth muscle proliferation by  
CC expressing cell cycle control genes or contraction inhibition peptides in  
CC smooth muscle cells, under the control of the SM22-alpha gene promoter  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;  
Query Match 30.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CWV 6  
Db |||  
2 CWV 4

```
RESULT 118
AAH26710/c
ID  AAH26710 standard; DNA; 10 BP.
XX
XX  AC  AAH26710;
XX
XX  DT  26-NOV-2001 (first entry)
XX
XX  DE  CARg box motif.
XX
XX  KW  CARg box; smooth muscle 22 alpha; SM22-alpha; promoter; mouse;
XX  KW  restenosis; atherosclerosis; asthma; cell proliferation; antiasthmatic;
XX  KW  antiarteriosclerotic; gene therapy; ss.
XX
XX  OS  Mammalia.
XX
XX  FN  USG284743-B1.
XX
XX  PD  04-SEP-2001.
XX
XX  PF  10-APR-2000; 2000US-00546550.
XX
XX  PR  05-OCT-1995; 95US-0004868P.
XX  PR  07-OCT-1996; 96US-00726807.
XX  PR  26-FEB-1999; 99US-00258367.
XX
XX  PA  (ARCH-) ARCH DEV CORP.
XX
XX  PI  Parmacek MS, Solway J;
XX  WIPI; 2001-588977/66.
XX
XX  PT  Modulating smooth muscle cell proliferation in a mammal, useful for
XX  PT  treating or preventing proliferation diseases, e.g. atherosclerosis,
XX  PT  restenosis or asthma, comprises contacting cells with smooth muscle 22
XX  PT  alpha gene promoter.
XX
XX  PS  Example 9; Col 34; 68pp; English.
XX
XX  CC  The present sequence is that of a CARg box motif. The motif is present in
XX  CC  smooth muscle elements 1 and 4 of the mouse smooth muscle 22 alpha (SM22-
XX  CC  alpha) gene promoter (see AAH26682). CARg boxes are involved in the
XX  CC  binding of the MADS box transcription factor SRF, and may play an
XX  CC  important role in regulating the transcription of genes encoding skeletal
XX  CC  and cardiac alpha-actin. The invention provides methods of preventing
XX  CC  restenosis following balloon angioplasty and methods of treating asthma.
XX  CC  The methods are based on inhibition of smooth muscle proliferation by
XX  CC  expressing cell cycle control genes or contraction inhibition peptides in
XX  CC  smooth muscle cells, under the control of the SM22-alpha gene promoter
XX
XX  SQ  Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

Query Match      30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 WVG 7
Db      |||
        4 WVG 2

RESULT 119
AAD20602
ID  AAD20602 standard; DNA; 10 BP.
XX
XX  AC  AAD20602;
XX
XX  DT  03-JAN-2002 (first entry)
XX
XX  DE  Consensus CARg box embedded in a smooth muscle element.
XX
XX  KW  Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
XX  KW  smooth muscle cell; proliferation; vasotropic; smooth muscle element;
XX  KW  SME; ds.
XX
XX  OS  Mus musculus.
XX  OS  Unidentified.
XX
XX  FN  USG291211-B1.
XX
XX  PD  18-SEP-2001.
XX
XX  PF  01-NOV-1999; 99US-00431414.
XX  PR  05-OCT-1995; 95US-0004868P.
XX

Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
smooth muscle cell; proliferation; vasotropic; smooth muscle element;
SME; ds.

Mus musculus.
Unidentified.

USG291211-B1.

18-SEP-2001.

01-NOV-1999; 99US-00431414.
05-OCT-1995; 95US-0004868P.

Query Match      30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CWV 6
Db      |||
        2 CWV 4

RESULT 120
AAD20602/c
ID  AAD20602 standard; DNA; 10 BP.
XX
XX  AC  AAD20602;
XX
XX  DT  03-JAN-2002 (first entry)
XX
XX  DE  Consensus CARg box embedded in a smooth muscle element.
XX
XX  KW  Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
XX  KW  smooth muscle cell; proliferation; vasotropic; smooth muscle element;
XX  KW  SME; ds.
XX
XX  OS  Mus musculus.
XX  OS  Unidentified.
XX
XX  FN  USG291211-B1.
XX
XX  PD  18-SEP-2001.
XX
XX  PF  01-NOV-1999; 99US-00431414.
XX  PR  05-OCT-1995; 95US-0004868P.
XX

Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
smooth muscle cell; proliferation; vasotropic; smooth muscle element;
SME; ds.

Mus musculus.
Unidentified.

USG291211-B1.

18-SEP-2001.

01-NOV-1999; 99US-00431414.
05-OCT-1995; 95US-0004868P.

Query Match      30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CWV 6
Db      |||
        2 CWV 4

RESULT 120
AAD20602/c
ID  AAD20602 standard; DNA; 10 BP.
XX
XX  AC  AAD20602;
XX
XX  DT  03-JAN-2002 (first entry)
XX
XX  DE  Consensus CARg box embedded in a smooth muscle element.
XX
XX  KW  Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
XX  KW  smooth muscle cell; proliferation; vasotropic; smooth muscle element;
XX  KW  SME; ds.
XX
XX  OS  Mus musculus.
XX  OS  Unidentified.
XX
XX  FN  USG291211-B1.
XX
XX  PD  18-SEP-2001.
XX
XX  PF  01-NOV-1999; 99US-00431414.
XX  PR  05-OCT-1995; 95US-0004868P.
XX

Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
smooth muscle cell; proliferation; vasotropic; smooth muscle element;
SME; ds.

Mus musculus.
Unidentified.

USG291211-B1.

18-SEP-2001.

01-NOV-1999; 99US-00431414.
05-OCT-1995; 95US-0004868P.

Query Match      30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CWV 6
Db      |||
        2 CWV 4
```

PR 07-OCT-1996; 96US-00726807.  
 XX (ARCH-) ARCH DEV CORP.  
 PA  
 XX Parmacek MS, Solway J;  
 PI  
 XX WPI; 2001-637950/73.  
 DR  
 XX Expressing a polypeptide other than a mouse SM22alpha in a cell, useful  
 PT in treating restenosis, by providing to the cell a nucleic acid construct  
 PT comprising an SM22alpha promoter operably linked to the sequence encoding  
 PT the polypeptide.  
 XX  
 XX Example 9; Col 33; 68pp; English.  
 PS  
 XX The present invention relates to a method for expressing a polypeptide  
 CC other than a mouse SM22alpha in a cell comprising providing to the cell a  
 CC nucleic acid construct having an SM22alpha promoter operably linked to a  
 CC nucleotide sequence encoding the polypeptide. The method is useful for  
 CC preventing restenosis following balloon angioplasty and treating asthma  
 CC based on inhibition of smooth muscle cell proliferation by expressing  
 CC cell cycle control genes. The present sequence is a consensus CarG box  
 CC embedded in a smooth muscle element (SME)  
 XX  
 XX Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;  
 SQ

Query Match 30.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CW 6  
 DB |||  
 9 CW 7

RESULT 121  
 AAD21142  
 ID AAD21142 standard; DNA; 10 BP.  
 XX  
 AC AAD21142;  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Consensus CarG box embedded in smooth muscle element (SME).  
 XX  
 KW Murine; vasotropic; cytostatic; angiogenesis; smooth muscle cell; SMC;  
 KW SM22 alpha; atherosclerosis; arterial injury; balloon angioplasty;  
 KW restenosis; airway blockage; asthma; proliferative disease; SME;  
 KW smooth muscle element; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN US6297221-B1.  
 XX  
 PD 02-OCT-2001.  
 XX  
 PF 05-JAN-1999; 99US-00225670.  
 XX  
 PR 05-OCT-1995; 95US-0004868P.  
 PR 07-OCT-1996; 96US-00726807.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 XX  
 PI Parmacek MS, Solway J;  
 XX  
 DR WPI; 2001-647294/74.  
 XX  
 PT Promoting angiogenesis and preventing atherosclerosis or restenosis  
 PT following balloon angioplasty, comprises providing to smooth muscle cell  
 PT nucleic acid construct containing an SM22 alpha promoter.  
 XX  
 XX Example 9; Col 33; 67pp; English.  
 PS  
 XX

CC The patent discloses a method for promoting angiogenesis in a mammal by  
 CC providing a nucleic acid construct comprising an SM22 alpha promoter to a  
 CC smooth muscle cell (SMC) in the mammal. The promoter is operably linked  
 CC to a nucleotide sequence encoding a polypeptide or RNA competent to  
 CC induce angiogenesis. The method is useful for promoting angiogenesis, for  
 CC preventing atherosclerosis, restenosis or other arterial injury following  
 CC balloon angioplasty and airway blockage in asthma. The promoter may be  
 CC used to express heterologous proteins or mRNAs in proliferating smooth  
 CC muscle cells and to control proliferative diseases, or to promote  
 CC angiogenesis. The present sequence is a consensus CarG box embedded in  
 CC nuclear protein binding sites, designated as smooth muscle element (SME).  
 CC This sequence binds to the MADS box transcription factor, SRF and play an  
 CC important role in regulating the transcription of genes encoding skeletal  
 CC and cardiac alpha actin  
 XX  
 XX Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;  
 SQ

Query Match 30.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CW 6  
 DB |||  
 2 CW 4

RESULT 122  
 AAD21142/c  
 ID AAD21142 standard; DNA; 10 BP.  
 XX  
 AC AAD21142;  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Consensus CarG box embedded in smooth muscle element (SME).  
 XX  
 KW Murine; vasotropic; cytostatic; angiogenesis; smooth muscle cell; SMC;  
 KW SM22 alpha; atherosclerosis; arterial injury; balloon angioplasty;  
 KW restenosis; airway blockage; asthma; proliferative disease; SME;  
 KW smooth muscle element; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN US6297221-B1.  
 XX  
 PD 02-OCT-2001.  
 XX  
 PF 05-JAN-1999; 99US-00225670.  
 XX  
 PR 05-OCT-1995; 95US-0004868P.  
 PR 07-OCT-1996; 96US-00726807.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 XX  
 PI Parmacek MS, Solway J;  
 XX  
 DR WPI; 2001-647294/74.  
 XX  
 PT Promoting angiogenesis and preventing atherosclerosis or restenosis  
 PT following balloon angioplasty, comprises providing to smooth muscle cell  
 PT nucleic acid construct containing an SM22 alpha promoter.  
 XX  
 XX Example 9; Col 33; 67pp; English.  
 PS  
 XX The patent discloses a method for promoting angiogenesis in a mammal by  
 CC providing a nucleic acid construct comprising an SM22 alpha promoter to a  
 CC smooth muscle cell (SMC) in the mammal. The promoter is operably linked  
 CC to a nucleotide sequence encoding a polypeptide or RNA competent to  
 CC induce angiogenesis. The method is useful for promoting angiogenesis, for  
 CC preventing atherosclerosis, restenosis or other arterial injury following  
 CC balloon angioplasty and airway blockage in asthma. The promoter may be  
 CC used to express heterologous proteins or mRNAs in proliferating smooth  
 CC muscle cells and to control proliferative diseases, or to promote

CC angiogenesis. The present sequence is a consensus CarG box embedded in  
 CC nuclear protein binding sites, designated as smooth muscle element (SME).  
 CC This sequence binds to the MADS box transcription factor, SRP and play an  
 CC important role in regulating the transcription of genes encoding skeletal  
 CC and cardiac alpha actin

XX  
 SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;  
 Query Match 30.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WNG 7  
 Db 4 WNG 2

## RESULT 123

AAD04664  
 ID AAD04664 standard; DNA; 10 BP.

XX AC AAD04664;

XX DT 04-JUL-2001 (first entry)

XX Thermus 9kb SphI fragment consensus direct repeat I of pTsp45L plasmid.

XX Replication protein; RepT; partition protein; ParA; pTsp45S plasmid;  
 KW kanamycin-resistance gene; thermophilic transformation; Ori;  
 KW replication origin; ds.

XX Thermus sp.

XX OS US6207377-B1.

XX PN 27-MAR-2001.

XX PF 14-AUG-1998; 98US-00134246.

XX PR 14-AUG-1998; 98US-00134246.

XX PA (NEWE ) NEW ENGLAND BIOLABS INC.

XX PI Wayne J, Xu S;

XX WPI; 2001-298939/31.

XX Cloning Thermus species (Ts) plasmid genes comprises transforming  
 PT Escherichia coli with cloned recombinant plasmid containing Ts and E.coli  
 PT origins of replication, isolating cloned recombinant plasmid from E.coli  
 PT and transforming Ts cell.

XX Example II; Col 8; 32pp; English.

XX The present DNA sequence is Thermus 9kb SphI fragment consensus direct  
 CC repeat I of pTsp45L plasmid. This 9kb SphI fragment encodes a partition  
 CC protein, parA gene. The direct repeat is important for pTsp45L plasmid  
 CC replication. The invention relates to Thermus sp. replication protein  
 CC Repr, partition protein ParA and their corresponding DNA molecules which  
 CC relates to recombinant DNA molecules encoding plasmid DNA replication  
 CC origins in Thermus, as well as to shuttle vectors which contain the same.  
 CC The invention also relates to method useful for cloning Thermus sp.

CC plasmid genes which comprises inserting plasmid DNA comprising a Thermus  
 CC sp. origin of replication (Ori) into a recombinant plasmid comprising a  
 CC thermostable kanamycin-resistance gene and an Escherichia coli Ori, to  
 CC produce a cloned recombinant plasmid. This cloned recombinant plasmid is  
 CC transformed with an E. coli. host cell, and E. coli. host cell cultured  
 CC for the expression of cloned recombinant plasmid. The cloned recombinant  
 CC plasmid isolated from E. coli host cell is then transformed with Thermus  
 CC sp. host cell and Thermus sp. host cell is cultured. Thus Thermus sp.  
 CC plasmid genes are cloned. These plasmid DNAs are used for thermophilic  
 CC transformation

XX

SQ Sequence 10 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
 Db 1 RRC 3

## RESULT 124

AAD04664/C  
 ID AAD04664 standard; DNA; 10 BP.

XX AC AAD04664;

XX DT 04-JUL-2001 (first entry)

XX Thermus 9kb SphI fragment consensus direct repeat I of pTsp45L plasmid.

XX Replication protein; RepT; partition protein; ParA; pTsp45S plasmid;  
 KW kanamycin-resistance gene; thermophilic transformation; Ori;  
 KW replication origin; ds.

XX Thermus sp.

XX OS US6207377-B1.

XX PN 27-MAR-2001.

XX PF 14-AUG-1998; 98US-00134246.

XX PR 14-AUG-1998; 98US-00134246.

XX PA (NEWE ) NEW ENGLAND BIOLABS INC.

XX PI Wayne J, Xu S;

XX WPI; 2001-298939/31.

XX Cloning Thermus species (Ts) plasmid genes comprises transforming  
 PT Escherichia coli with cloned recombinant plasmid containing Ts and E.coli  
 PT origins of replication, isolating cloned recombinant plasmid from E.coli  
 PT and transforming Ts cell.

XX Example II; Col 8; 32pp; English.

XX The present DNA sequence is Thermus 9kb SphI fragment consensus direct  
 CC repeat I of pTsp45L plasmid. This 9kb SphI fragment encodes a partition  
 CC protein, parA gene. The direct repeat is important for pTsp45L plasmid  
 CC replication. The invention relates to Thermus sp. replication protein  
 CC Repr, partition protein ParA and their corresponding DNA molecules which  
 CC relates to recombinant DNA molecules encoding plasmid DNA replication  
 CC origins in Thermus, as well as to shuttle vectors which contain the same.  
 CC The invention also relates to method useful for cloning Thermus sp.

CC plasmid genes which comprises inserting plasmid DNA comprising a Thermus  
 CC sp. origin of replication (Ori) into a recombinant plasmid comprising a  
 CC thermostable kanamycin-resistance gene and an Escherichia coli Ori, to  
 CC produce a cloned recombinant plasmid. This cloned recombinant plasmid is  
 CC transformed with an E. coli. host cell, and E. coli. host cell cultured  
 CC for the expression of cloned recombinant plasmid. The cloned recombinant  
 CC plasmid isolated from E. coli host cell is then transformed with Thermus  
 CC sp. host cell and Thermus sp. host cell is cultured. Thus Thermus sp.  
 CC plasmid genes are cloned. These plasmid DNAs are used for thermophilic  
 CC transformation

SQ Sequence 10 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 RRR 3
      |||
Db     10 RRR 8

RESULT 125
ABK33367
ID ABK33367 standard; DNA; 10 BP.
XX
AC ABK33367;
XX
DT 08-MAY-2002 (first entry)
XX
DE SRF binding site or CARg box.
XX
KW SM22alpha; smooth muscle cell specific protein; ds; vasotropic;
KW antiasthmatic; muscular; bioprostheses; EMSA; gene therapy;
KW electrophoretic mobility shift assay; restenosis; balloon angioplasty;
KW arterial injury; angiogenesis; graft; stent implant; asthma;
KW smooth muscle cell proliferative disease;
KW transcription factor binding site.
XX
OS Mammalia.
XX
PN US6331527-B1.
XX
PD 18-DEC-2001.
XX
PF 01-NOV-1999; 99US-00431349.
XX
PR 05-OCT-1995; 95US-0004868P.
PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2002-129550/17.
XX
PT A bioprostheses for use in the prevention of restenosis and in the
PT prevention and treatment of smooth muscle cell proliferative diseases
PT comprises a smooth muscle cell transfected with an SM22-alpha promoter
PT operably linked to a DNA sequence.
XX
PS Example 9; Col 33; 69pp; English.
XX
CC The invention relates to a bioprostheses comprises a smooth muscle cell
CC transfected with a nucleic acid segment comprising an SM22alpha promoter
CC region operably linked to a DNA sequence encoding a molecule other than
CC mouse SM22alpha (a smooth muscle specific protein). Also included are a
CC method of providing a molecule of interest to a blood vessel in a mammal
CC by providing a bioprostheses comprising, placing in a blood vessel and
CC obtaining expression and a method of providing a molecule of interest to
CC a blood vessel in a mammal by providing a bioprostheses comprising an
CC oligomer comprising SME1 - SME6, corresponding to the EMSA
CC (electrophoretic mobility shift assay) appearing as ABK33341, ABK33343,
CC ABK33345, ABK33347 ABK33351 and ABK33353 or a sequence that hybridizes
CC with the complement of the above sequences, placing in a blood vessel and
CC obtaining expression. The bioprostheses can be used in methods to provide
CC a molecule of interest to a blood vessel in a mammal (i.e by gene
CC therapy). It can also be used in the prevention of restenosis following
CC balloon angioplasty or other arterial injury, in the promotion of
CC angiogenesis in graft or stent implants and in the treatment or
CC prevention of asthma along with other smooth muscle cell proliferative
CC diseases. The control of expression of the smooth muscle cell specific
CC promoter is constitutive and cell cycle independent, it thus promotes
CC transcription in both resting and proliferating cells in contrast to
CC other known smooth muscle cell promoters that are down regulated in
CC proliferating cells. The present sequence is a transcription factor
CC binding site sequence found in SM22alpha or related genes
XX
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;
```

Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6  
Db 2 CWW 4

RESULT 126  
ABK33367/c  
ID ABK33367 standard; DNA; 10 BP.  
XX  
AC ABK33367;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE SRF binding site or CARg box.  
XX  
KW SM22alpha; smooth muscle cell specific protein; ds; vasotropic;  
KW antiasthmatic; muscular; bioprostheses; EMSA; gene therapy;  
KW electrophoretic mobility shift assay; restenosis; balloon angioplasty;  
KW arterial injury; angiogenesis; graft; stent implant; asthma;  
KW smooth muscle cell proliferative disease;  
KW transcription factor binding site.  
XX  
OS Mammalia.  
XX  
PN US6331527-B1.  
XX  
PD 18-DEC-2001.  
XX  
PF 01-NOV-1999; 99US-00431349.  
XX  
PR 05-OCT-1995; 95US-0004868P.  
PR 07-OCT-1996; 96US-00726807.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Parmacek MS, Solway J;  
XX  
DR WPI; 2002-129550/17.  
XX  
PT A bioprostheses for use in the prevention of restenosis and in the  
PT prevention and treatment of smooth muscle cell proliferative diseases  
PT comprises a smooth muscle cell transfected with an SM22-alpha promoter  
PT operably linked to a DNA sequence.  
XX  
PS Example 9; Col 33; 69pp; English.  
XX  
CC The invention relates to a bioprostheses comprises a smooth muscle cell  
CC transfected with a nucleic acid segment comprising an SM22alpha promoter  
CC region operably linked to a DNA sequence encoding a molecule other than  
CC mouse SM22alpha (a smooth muscle specific protein). Also included are a  
CC method of providing a molecule of interest to a blood vessel in a mammal  
CC by providing a bioprostheses comprising, placing in a blood vessel and  
CC obtaining expression and a method of providing a molecule of interest to  
CC a blood vessel in a mammal by providing a bioprostheses comprising an  
CC oligomer comprising SME1 - SME6, corresponding to the EMSA  
CC (electrophoretic mobility shift assay) appearing as ABK33341, ABK33343,  
CC ABK33345, ABK33347 ABK33351 and ABK33353 or a sequence that hybridizes  
CC with the complement of the above sequences, placing in a blood vessel and  
CC obtaining expression. The bioprostheses can be used in methods to provide  
CC a molecule of interest to a blood vessel in a mammal (i.e by gene  
CC therapy). It can also be used in the prevention of restenosis following  
CC balloon angioplasty or other arterial injury, in the promotion of  
CC angiogenesis in graft or stent implants and in the treatment or  
CC prevention of asthma along with other smooth muscle cell proliferative  
CC diseases. The control of expression of the smooth muscle cell specific  
CC promoter is constitutive and cell cycle independent, it thus promotes  
CC transcription in both resting and proliferating cells in contrast to  
CC other known smooth muscle cell promoters that are down regulated in  
CC proliferating cells. The present sequence is a transcription factor  
CC binding site sequence found in SM22alpha or related genes



CC binding site sequence found in SM22alpha or related genes  
 XX  
 SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 WWG 7  
 DB 4 WWG 2

## RESULT 127

ABK85627  
 ID ABK85627 standard; DNA; 10 BP.

XX  
 AC ABK85627;

XX  
 DT 16-AUG-2002 (first entry)

XX Serum responsive element (SRE) consensus sequence.

XX NET; ss; ERP; SAP-1; angiogenesis; transgenic; ulcer; SRE; gel-shift;  
 KW ischaemia; wound healing; vascular restenosis; hypertension; dementia;  
 KW alzheimer's disease; lymphoedema; atherosclerosis; haemangioma; bone;  
 KW haemangi endotheloma; ovarian hyperstimulation; endometriosis; ascites;  
 KW follicular cyst; Kaposi sarcoma; tumour; cancer; allergy; synovitis;  
 KW respiratory distress; rheumatoid arthritis; pneumonia; thyroiditis;  
 KW cartilage dysfunction; obesity; asthma; inflammation; hepatitis;  
 KW glomerulonephritis; diabetic retinopathy; thyroiditis; nasal polyp;  
 KW serum response element.

XX Unidentified.

XX EPI202065-A1.

XX 02-MAY-2002.

XX 25-OCT-2000; 2000EP-00402968.

XX 25-OCT-2000; 2000EP-00402968.

XX (AVET ) AVENTIS PHARMA SA.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX Wasylyk B, Multon M, Ayadi A, Zheng H;

XX WPI; 2002-437317/47.

XX Use of all or part of a NET polypeptide to identify compounds useful to  
 PT modulate angiogenesis and prevent or treat pathologies associated with  
 PT angiogenic disorders e.g. cardiac ischemia, atherosclerosis or tumor  
 PT growth.

XX Disclosure; Page 2; 77pp; English.

XX This invention relates to the use of all or part of a NET (also known as  
 CC ERP or SAP-1) polypeptide to identify compounds modulating angiogenesis  
 CC or compounds that can be used to prevent or treat pathologies associated  
 CC with angiogenic disorders. The invention also comprises transgenic  
 CC animals that bear mutations in the NET gene. The method and transgenic  
 CC animals of the invention are useful to identify compounds to treat  
 CC pathologies associated with angiogenic disorders involving insufficient  
 CC vascularisation and requiring increased angiogenesis (e.g. cardiac/  
 CC peripheral ischaemia, defects in wound healing and vascular restenosis,  
 CC hypertension, ulcers, alzheimer's disease, lymphoedema, dementia) or  
 CC involving increased vascularisation and requiring decreased angiogenesis  
 CC (e.g. atherosclerosis, haemangioma, haemangi endotheloma, ovarian  
 CC hyperstimulation, endometriosis, ascites, follicular cysts, ). They are  
 CC also useful to identify compounds useful to treat pathologies associated  
 CC with angiogenic disorders such as Kaposi sarcoma, tumour growth and  
 CC cancer, or other pathologies in which NET is activated). Such compounds

CC may also be used to treat allergies, dysfunctional uterine bleeding,  
 CC respiratory distress, rheumatoid arthritis, bone and cartilage  
 CC dysfunction, obesity, synovitis, inflammation, hepatitis.  
 CC glomerulonephritis, asthma, retinopathy, thyroiditis, pneumonia, nasal  
 CC polyps and thyroiditis. Such compounds may be e.g. antisense  
 CC polynucleotides downregulating or blocking expression of a NET gene,  
 CC intracellular binding proteins or NET dominant negative mutants.  
 CC Compounds modulating NET activity may also be included in medicaments to  
 CC prevent and/or treat pathologies associated with angiogenic disorders.  
 CC The present sequence represents a serum responsive element (SRE)  
 CC consensus sequence shown in the specification

XX SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CWG 6

DB 2 CWG 4

## RESULT 128

ABK85627/c

ID ABK85627 standard; DNA; 10 BP.

XX  
 XX ABK85627;

XX 16-AUG-2002 (first entry)

XX Serum responsive element (SRE) consensus sequence.

XX NET; ss; ERP; SAP-1; angiogenesis; transgenic; ulcer; SRE; gel-shift;  
 KW ischaemia; wound healing; vascular restenosis; hypertension; dementia;  
 KW alzheimer's disease; lymphoedema; atherosclerosis; haemangioma; bone;  
 KW haemangi endotheloma; ovarian hyperstimulation; endometriosis; ascites;  
 KW follicular cyst; Kaposi sarcoma; tumour; cancer; allergy; synovitis;  
 KW respiratory distress; rheumatoid arthritis; pneumonia; thyroiditis;  
 KW cartilage dysfunction; obesity; asthma; inflammation; hepatitis;  
 KW glomerulonephritis; diabetic retinopathy; thyroiditis; nasal polyp;  
 KW serum response element.

XX Unidentified.

XX EPI202065-A1.

XX 02-MAY-2002.

XX 25-OCT-2000; 2000EP-00402968.

XX 25-OCT-2000; 2000EP-00402968.

XX (AVET ) AVENTIS PHARMA SA.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX Wasylyk B, Multon M, Ayadi A, Zheng H;

XX WPI; 2002-437317/47.

XX Use of all or part of a NET polypeptide to identify compounds useful to  
 PT modulate angiogenesis and prevent or treat pathologies associated with  
 PT angiogenic disorders e.g. cardiac ischemia, atherosclerosis or tumor  
 PT growth.

XX Disclosure; Page 2; 77pp; English.

XX This invention relates to the use of all or part of a NET (also known as  
 CC ERP or SAP-1) polypeptide to identify compounds modulating angiogenesis  
 CC or compounds that can be used to prevent or treat pathologies associated  
 CC with angiogenic disorders. The invention also comprises transgenic  
 CC animals that bear mutations in the NET gene. The method and transgenic  
 CC animals of the invention are useful to identify compounds to treat

pathologies associated with angiogenic disorders involving insufficient vascularisation and requiring increased angiogenesis (e.g. cardiac/peripheral ischaemia, defects in wound healing and vascular restenosis, hypertension, ulcers, Alzheimer's disease, lymphoedema, dementia) or involving increased vascularisation and requiring decreased angiogenesis (e.g. atherosclerosis, haemangioma, haemangioendothelioma, ovarian hyperstimulation, endometriosis, ascites, follicular cysts, ). They are also useful to identify compounds useful to treat pathologies associated with angiogenic disorders such as Kaposi sarcoma, tumour growth and cancer, or other pathologies in which NET is activated). Such compounds may also be used to treat allergies, dysfunctional uterine bleeding, respiratory distress, rheumatoid arthritis, bone and cartilage dysfunction, obesity, synovitis, inflammation, hepatitis, glomerulonephritis, asthma, retinopathy, thyroiditis, pneumonia, nasal polyps and thyroiditis. Such compounds may be e.g. antisense polynucleotides downregulating or blocking expression of a NET gene, intracellular binding proteins or NET dominant negative mutants. Compounds modulating NET activity may also be included in medicaments to prevent and/or treat pathologies associated with angiogenic disorders. The present sequence represents a serum responsive element (SRE) consensus sequence shown in the specification

SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6  
DB 9 CWV 7

## RESULT 129

ABL53549  
ID ABL53549 standard; DNA; 10 BP.

AC ABL53549;

DT 10-JUN-2002 (first entry)

DE CpG motif.

KW CpG; autoimmune disease; insulin dependent diabetes mellitus; IDDM;  
KW DNA immunisation; vaccine; antidiabetic; immunotherapy; gene therapy; ss.

OS Synthetic.

PN WO200216549-A2.

PD 28-FEB-2002.

PF 23-AUG-2001; 2001WO-IL000790.

PR 25-AUG-2000; 2000US-0227853P.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Cohen IR, Quintana FJ;

DR WPI; 2002-227369/28.

PT Treating or preventing an ongoing autoimmune disease e.g. diabetes,  
PT comprises vaccination with a DNA sequence comprising a CpG motif.

PS Disclosure; Page 9; 53pp; English.

The present sequence is that of an example of a CpG motif. The invention relates to methods for the prevention or treatment of autoimmune disease, particularly insulin dependent diabetes mellitus (IDDM). A DNA vaccine which includes a CpG motif, such as that given in the CpG oligonucleotide of ABL53541, is preferably used. The vaccine may also include DNA encoding an antigen associated with the autoimmune disease

XX SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;  
Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
DB 1 RRC 3

## RESULT 130

ABL53549/c  
ID ABL53549 standard; DNA; 10 BP.

AC ABL53549;

DT 10-JUN-2002 (first entry)

DE CpG motif.

KW CpG; autoimmune disease; insulin dependent diabetes mellitus; IDDM;  
KW DNA immunisation; vaccine; antidiabetic; immunotherapy; gene therapy; ss.

OS Synthetic.

PN WO200216549-A2.

PD 28-FEB-2002.

PF 23-AUG-2001; 2001WO-IL000790.

PR 25-AUG-2000; 2000US-0227853P.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Cohen IR, Quintana FJ;

DR WPI; 2002-227369/28.

PT Treating or preventing an ongoing autoimmune disease e.g. diabetes,  
PT comprises vaccination with a DNA sequence comprising a CpG motif.

PS Disclosure; Page 9; 53pp; English.

The present sequence is that of an example of a CpG motif. The invention relates to methods for the prevention or treatment of autoimmune disease, particularly insulin dependent diabetes mellitus (IDDM). A DNA vaccine which includes a CpG motif, such as that given in the CpG oligonucleotide of ABL53541, is preferably used. The vaccine may also include DNA encoding an antigen associated with the autoimmune disease

SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
DB 10 RRC 8

## RESULT 131

ADG88268  
ID ADG88268 standard; DNA; 10 BP.

AC ADG88268;

DT 22-APR-2004 (first entry)

XX Pathogen infection-related gene consensus motif 1 cis element #710.



Db 6 WWG 4

RESULT 133  
ABZ24785

ID ABZ24785 standard; DNA; 10 BP.  
AC  
XX  
DT 07-APR-2003 (first entry)  
XX  
AC ABZ24785;  
XX  
DT 07-APR-2003 (first entry)  
XX  
DE Oligodeoxynucleic acid molecule ODN 16-A.  
XX  
KW Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;  
KW ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "thiophosphate backbone"  
XX  
PN WO200295027-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 17-MAY-2002; 2002WO-EP005448.  
XX  
PR 21-MAY-2001; 2001AT-00000805.  
XX  
PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
XX  
PI Lingnau K, Schellack C, Schmidt W;  
XX  
DR WPI; 2003-183880/18.  
XX  
PT New oligodeoxynucleic acid molecules useful for the preparation of  
PT vaccine.  
XX  
PS Example 9; Page 35; 57pp; English.  
XX  
CC The present sequence is that of a thiosubstituted oligodeoxynucleic acid  
CC molecule, ODN 16-A, including a deoxyuridine monophosphate. The invention  
CC is based on the discovery that ODNs containing deoxyuridine residues (U-  
CC ODNs) have an immunostimulatory effect comparable to, or in many  
CC instances greater than, ODNs containing CpG motifs, producing higher  
CC numbers of specific T cells to a given antigen. The U-ODNs do not induce  
CC the systemic production of pro-inflammatory cytokines and, in contrast to  
CC CpG ODNs, are not dependent on a specific motif or a palindromic  
CC sequence. Use of a U-ODN for the preparation of a vaccine is claimed.  
CC Combining the U-ODN with an antigen strongly increases the potential of  
CC the antigen to raise the protection/immune response of a vaccinated  
CC individual. An example of the invention demonstrated the generation of a  
CC specific immune response against a melanoma-derived peptide (see  
CC ABP58360) by injection of mice with the peptide in combination with ODN  
CC 16-A  
SQ Sequence 10 BP; 0 A; 0 C; 0 G; 1 T; 1 U; 8 Other;  
Query Match 30.0%; Score 3; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 134  
ABZ24785/c

ID ABZ24785 standard; DNA; 10 BP.  
XX  
AC ABZ24785;  
XX  
DT 07-APR-2003 (first entry)  
XX  
DE Oligodeoxynucleic acid molecule ODN 16-A.  
XX  
KW Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;  
KW ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "thiophosphate backbone"  
XX  
PN WO200295027-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 17-MAY-2002; 2002WO-EP005448.  
XX  
PR 21-MAY-2001; 2001AT-00000805.  
XX  
PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
XX  
PI Lingnau K, Schellack C, Schmidt W;  
XX  
DR WPI; 2003-183880/18.  
XX  
PT New oligodeoxynucleic acid molecules useful for the preparation of  
PT vaccine.  
XX  
PS Example 9; Page 35; 57pp; English.  
XX  
CC The present sequence is that of a thiosubstituted oligodeoxynucleic acid  
CC molecule, ODN 16-A, including a deoxyuridine monophosphate. The invention  
CC is based on the discovery that ODNs containing deoxyuridine residues (U-  
CC ODNs) have an immunostimulatory effect comparable to, or in many  
CC instances greater than, ODNs containing CpG motifs, producing higher  
CC numbers of specific T cells to a given antigen. The U-ODNs do not induce  
CC the systemic production of pro-inflammatory cytokines and, in contrast to  
CC CpG ODNs, are not dependent on a specific motif or a palindromic  
CC sequence. Use of a U-ODN for the preparation of a vaccine is claimed.  
CC Combining the U-ODN with an antigen strongly increases the potential of  
CC the antigen to raise the protection/immune response of a vaccinated  
CC individual. An example of the invention demonstrated the generation of a  
CC specific immune response against a melanoma-derived peptide (see  
CC ABP58360) by injection of mice with the peptide in combination with ODN  
CC 16-A  
SQ Sequence 10 BP; 0 A; 0 C; 0 G; 1 T; 1 U; 8 Other;  
Query Match 30.0%; Score 3; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 10 RRR 8

RESULT 135  
ADJ56890

ID ADJ56890 standard; DNA; 10 BP.  
XX  
AC ADJ56890;  
XX  
DT 06-MAY-2004 (first entry)



XX WPI; 2004-400165/37.  
 XX  
 PT New agent that modulates megakaryocytic acute leukemia (MAL) activity,  
 PT useful for combating e.g., cancer, particularly acute myeloid leukemia  
 PT (AML-M7), wounds, or myopathies such as muscle hypertrophy.  
 XX  
 PS Disclosure; SEQ ID NO 1; 143pp; English.  
 XX  
 CC The invention relates to an agent that modulates a megakaryocytic acute  
 CC leukemia (MAL) activity. The agent or the polynucleotide that encodes the  
 CC agent is useful for combating a disorder in an individual by modulating  
 CC (either inhibiting or stimulating) a MAL activity, where the disorder is  
 CC cancer such as leukemia, particularly childhood leukemia AML-M7, wounds,  
 CC myopathies such as muscle hypertrophy, and any disorder that would  
 CC benefit from enhanced angiogenesis. In cancer, the agent combats tumor  
 CC cell growth, adhesion, cellular mobility, invasion or metastasis. The  
 CC polynucleotide that encodes the agent is useful in medicine and in the  
 CC manufacture of a medicament for combating the disorders above. The  
 CC agents, its encoding polynucleotide or the genetic construct is useful  
 CC for modulating an activity of MAL in vitro. This sequence corresponds to  
 CC the SRF binding site used in the method of the invention.  
 XX  
 SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;  
 Query Match 30.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CWW 6  
 Db |||  
 2 CWW 4  
 RESULT 138  
 ADN98340/c  
 ID ADN98340 standard; DNA; 10 BP.  
 XX  
 AC ADN98340;  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Serum response factor binding sequence.  
 XX  
 KW ss; cytostatic; vulnarary; muscular;  
 KW megakaryocytic acute leukemia modulator; MAL modulator; MAL stimulator;  
 KW MAL inhibitor; MAL binding agent; serum response factor modulator;  
 KW SRF modulator; SRF stimulator; SRF inhibitor; SRF binding agent;  
 KW actin binding agent; antisense; RNAi; megakaryocytic acute leukemia;  
 KW cancer; leukemia; wounds; myopathy; muscle hypertrophy; angiogenesis;  
 KW metastasis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004039980-A1.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-GB004674.  
 XX  
 PR 30-OCT-2002; 2002US-0422420P.  
 XX  
 PA (CANC-) CANCER RES TECHNOLOGY LTD.  
 XX  
 XX Treisman RH, Miralles-Arenas F, Zaromytidou A, Posern G;  
 XX  
 XX WPI; 2004-400165/37.  
 XX  
 PT New agent that modulates megakaryocytic acute leukemia (MAL) activity,  
 PT useful for combating e.g., cancer, particularly acute myeloid leukemia  
 PT (AML-M7), wounds, or myopathies such as muscle hypertrophy.  
 XX

PS Disclosure; SEQ ID NO 1; 143pp; English.  
 XX  
 CC The invention relates to an agent that modulates a megakaryocytic acute  
 CC leukemia (MAL) activity. The agent or the polynucleotide that encodes the  
 CC agent is useful for combating a disorder in an individual by modulating  
 CC (either inhibiting or stimulating) a MAL activity, where the disorder is  
 CC cancer such as leukemia, particularly childhood leukemia AML-M7, wounds,  
 CC myopathies such as muscle hypertrophy, and any disorder that would  
 CC benefit from enhanced angiogenesis. In cancer, the agent combats tumor  
 CC cell growth, adhesion, cellular mobility, invasion or metastasis. The  
 CC polynucleotide that encodes the agent is useful in medicine and in the  
 CC manufacture of a medicament for combating the disorders above. The  
 CC agents, its encoding polynucleotide or the genetic construct is useful  
 CC for modulating an activity of MAL in vitro. This sequence corresponds to  
 CC the SRF binding site used in the method of the invention.  
 XX  
 SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;  
 Query Match 30.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 CWW 6  
 Db |||  
 9 CWW 7  
 RESULT 139  
 AAT96077  
 ID AAT96077 standard; DNA; 11 BP.  
 XX  
 AC AAT96077;  
 DT 31-MAR-1998 (first entry)  
 XX  
 DE Recombination region homologous to SINE flanking region.  
 XX  
 KW Recombination region; consensus defined flanking region;  
 KW short interspersed repeated DNA element; SINE; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5695977-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 07-MAY-1996; 96US-00643886.  
 XX  
 PR 31-AUG-1995; 95US-0003063P.  
 XX  
 PA (GENE-) GENETIC INFORMATION RES INST.  
 XX  
 XX Jurka JW;  
 XX  
 XX WPI; 1998-0411303/04.  
 XX  
 PT Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 PS Claim 7; Col 17-18; 12pp; English.  
 XX  
 CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen

CC cosmetics, foods and drugs. By using antisense sequences effective  
CC inhibition of both copies of a gene is possible, ensuring the substantial  
CC absence of the particular transcriptional or translational product. In  
CC addition the method may enhance efficiency in gene therapy, when  
CC providing for a capability in which the host is deficient

XX Sequence 11 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3

Db 8 RRR 10

RESULT 140

AAT96077/C

ID AAT96077 standard; DNA; 11 BP.

XX AC AAT96077;

XX DT 31-MAR-1998 (first entry)

XX DE Recombination region homologous to SINE flanking region.

XX KW Recombination region; consensus defined flanking region;

XX KW short interspersed repeated DNA element; SINE; ss.

XX OS Synthetic.

XX PN US5695977-A.

XX PD 09-DEC-1997.

XX PF 07-MAY-1996; 96US-00643886.

XX PR 31-AUG-1995; 95US-0003063P.

XX PA (GENE-) GENETIC INFORMATION RES INST.

XX PI Jurka JW;

XX DR WPI; 1998-041303/04.

XX PT Genomic integration of DNA by site directed recombination - using  
XX PT construct containing recombination region homologous to consensus defined  
XX PT flanking region of short interspersed repeated DNA element.

XX PS Claim 7; Col 17-18; 12pp; English.

XX CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
XX CC comprises introducing a construct comprising the DNA sequence and a  
XX CC recombination region homologous to a consensus defined flanking region of  
XX CC a short interspersed repeated DNA element (SINE), e.g. the present  
XX CC sequence. The method may be used to modify the phenotype of cells, or  
XX CC investigate the response of receptors, metabolic pathways or expression  
XX CC products involved in the regulation of transcription or transduction of  
XX CC signals. It may also be used to produce protein products and transgenic  
XX CC animals, by providing novel capabilities to the cells or inhibiting  
XX CC endogenous capabilities, investigate physiological indications and screen  
XX CC cosmetics, foods and drugs. By using antisense sequences effective  
XX CC inhibition of both copies of a gene is possible, ensuring the substantial  
XX CC absence of the particular transcriptional or translational product. In  
XX CC addition the method may enhance efficiency in gene therapy, when  
XX CC providing for a capability in which the host is deficient

XX SQ Sequence 11 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10

Db 10 YYY 8

RESULT 141

ABA94933

XX ID ABA94933 standard; DNA; 11 BP.

XX AC ABA94933;

XX DT 08-MAY-2002 (first entry)

XX DE Human ecNOS gene nuclear factor Y (NFY\_Q6) binding site DNA fragment.

XX KW Single nucleotide polymorphism; SNP; ecNOS; cytostatic; anti-diabetic;  
XX KW endothelial consecutive nitric oxide synthase; nephrotropic; hypotensive;  
XX KW cardiant; anti-atherosclerotic; vasoconstrictor; ophthalmological; human;  
XX KW tranquilizer; anxiolytic; anti-asthmatic; sedative; antiinflammatory;  
XX KW anticoagulant; osteopathic; cancer; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT variation 8

XX FT /\*tag= a  
XX FT /note= "SNP replaces the G in the core binding site with  
XX FT an A at this position"

XX PN WO200208467-A1.

XX PD 31-JAN-2002.

XX PF 25-JUL-2001; 2001WO-US023321.

XX PR 25-JUL-2000; 2000US-0220662P.

XX PA (DZGE-) DZ GENES LLC.

XX PI Moskowitz DW;

XX DR WPI; 2002-188635/24.

XX PT Diagnosing a genetic susceptibility for a disease, condition, or disorder  
XX PT in a subject comprises detecting the presence of a single nucleotide  
XX PT polymorphism in the endothelial consecutive nitric oxide synthase gene.

XX PS Example 5; Page 74; 97pp; English.

XX CC The invention relates to diagnosing a genetic susceptibility for a  
XX CC disease, condition, or disorder in a subject that comprises analysing a  
XX CC nucleic acid in a biological sample to detect the presence of a single  
XX CC nucleotide polymorphism (SNP) in the endothelial consecutive nitric oxide  
XX CC synthase (ecNOS) gene. The SNP is associated with a disease, condition or  
XX CC disorder selected from breast cancer, lung cancer, prostate cancer, non-  
XX CC insulin dependent diabetes, end stage renal disease due to non-insulin  
XX CC dependent diabetes or hypertension, hypertension, myocardial infarction,  
XX CC colon cancer, atherosclerotic peripheral vascular disease, cataracts,  
XX CC cerebrovascular accident, cardiomyopathy with hypertension, ischaemic  
XX CC cardiomyopathy, atrial fibrillation without valvular disease, alcohol  
XX CC abuse, anxiety, asthma, cholecystectomy, chronic obstructive pulmonary  
XX CC disease, degenerative joint disease and frequent de-clots and seizure  
XX CC disorder. The method is useful for diagnosing a genetic predisposition to  
XX CC a disease associated with SNPs, for designing a treatment regimen for a  
XX CC patient having a disease, condition or disorder caused either directly or  
XX CC indirectly by the presence of one or more SNPs. The present sequence  
XX CC represents the human ecNOS gene fragment where a polymorphism can occur

XX SQ Sequence 11 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 30.0%; Score 3; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
|  
|  
|  
Db 8 GY 10

RESULT 142  
ABA94933/C  
ID ABA94933 standard; DNA; 11 BP.  
XX  
AC ABA94933;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human eCNOS gene nuclear factor Y (NFY\_Q6) binding site DNA fragment.  
XX  
KW Single nucleotide polymorphism; SNP; eCNOS; cytostatic; anti-diabetic;  
KW endothelial consecutive nitric oxide synthase; nephrotropic; hypotensive;  
KW cardiant; anti-atherosclerotic; vasoconstrictor; ophthalmological; human;  
KW tranquilizer; anxiolytic; anti-asthmatic; sedative; antiinflammatory;  
KW anticoagulant; osteopathic; cancer; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation 8  
FT /\*tag= a  
FT /note= "SNP replaces the G in the core binding site with  
FT an A at this position"  
XX  
PN WO200208467-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 25-JUL-2001; 2001WO-US023321.  
XX  
PR 25-JUL-2000; 2000US-0220662P.  
XX  
PA (DZGE-) DZ GENES LLC.  
XX  
PI Moskowitz DW;  
XX  
DR WPI; 2002-188635/24.  
XX  
PT Diagnosing a genetic susceptibility for a disease, condition, or disorder  
PT in a subject comprises detecting the presence of a single nucleotide  
PT polymorphism in the endothelial consecutive nitric oxide synthase gene.  
XX  
PS Example 5; Page 74; 97pp; English.  
XX  
CC The invention relates to diagnosing a genetic susceptibility for a  
CC disease, condition, or disorder in a subject that comprises analyzing a  
CC nucleic acid in a biological sample to detect the presence of a single  
CC nucleotide polymorphism (SNP) in the endothelial consecutive nitric oxide  
CC synthase (eCNOS) gene. The SNP is associated with a disease, condition or  
CC disorder selected from breast cancer, lung cancer, prostate cancer, non-  
CC insulin dependent diabetes, end stage renal disease due to non-insulin  
CC dependent diabetes or hypertension, hypertension, myocardial infarction,  
CC colon cancer, atherosclerotic peripheral vascular disease, cataracts,  
CC cerebrovascular accident, cardiomyopathy with hypertension, ischaemic  
CC cardiomyopathy, atrial fibrillation without valvular disease, alcohol  
CC abuse, anxiety, asthma, cholecystectomy, chronic obstructive pulmonary  
CC disease, degenerative joint disease and frequent de-clots and seizure  
CC disorder. The method is useful for diagnosing a genetic predisposition to  
CC a disease associated with SNPs, for designing a treatment regimen for a  
CC patient having a disease, condition or disorder caused either directly or  
CC indirectly by the presence of one or more SNPs. The present sequence  
CC represents the human eCNOS gene fragment where a polymorphism can occur  
XX  
SQ Sequence 11 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|  
|  
|  
Db 10 RRC 8

RESULT 143  
ADJ71749  
ID ADJ71749 standard; DNA; 11 BP.  
XX  
AC ADJ71749;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Aptamer peptide display library inserted sequence end.  
XX  
KW cytostatic; analgesic; anticonvulsant; cerebroprotective;  
KW antiparkinsonian; nootropic; neuroprotective; anti-HIV;  
KW modulator of cell phenotype; gene therapy; peptide aptamer;  
KW cell phenotype modification; peptide display library; cancer; pain;  
KW epilepsy; stroke; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; multiple sclerosis; AIDS; ds; Gene; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003040168-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 06-NOV-2002; 2002WO-US035584.  
XX  
PR 06-NOV-2001; 2001US-0333262P.  
XX  
PR 14-FEB-2002; 2002US-0357278P.  
XX  
PA (ENAN-) ENANTA PHARM INC.  
XX  
PI Benson JD, Vincent SM, Brasher BB, Miao Z, Lamming D;  
XX  
DR WPI; 2003-541418/51.  
XX  
PT Identifying peptide aptamer capable of modifying cell phenotype, by  
PT contacting cell sample with library encoding random peptide aptamers,  
PT selecting cell with altered phenotype, and identifying aptamers expressed  
PT in cell.  
XX  
PS Example 1; SEQ ID NO 5; 173pp; English.  
XX  
CC The invention relates to a method of identifying (M1) a peptide aptamer  
CC (PA) capable of modifying a cell phenotype, involving contacting a list  
CC sample of cells with a library of expressible nucleic acid sequences  
CC encoding random peptide aptamers linked to a fusion moiety, selecting at  
CC least one cell having an altered phenotype compared to the phenotype of  
CC the cell prior to contacting, and identifying peptide aptamers expressed  
CC in the selected cell. PA, its derivative or corresponding nucleic acid is  
CC useful for the molecular modelling of an agent having similar binding  
CC characteristics as PA. PA, its derivative or corresponding expressible  
CC nucleic acid is useful for treating or inhibiting a disease or condition  
CC (such as cancer) associated with an aberrant cell phenotype in a subject,  
CC where the aberrant cell phenotype is associated with a change in levels  
CC of apoptosis, viral resistance, signal transduction, protein trafficking,  
CC cell adhesion, membrane transport, cell motility, metabolic state or  
CC differentiation, when compared to a control cell, or the aberrant cell  
CC phenotype is associated with a tumor cell. The expressible nucleic acid  
CC is administered using a retrovirus that comprises a chromatin insulator  
CC element. PA is useful as a prognostic or diagnostic tool, for altering a  
CC cell phenotype, in gene therapy, as therapeutics for treating diseases  
CC (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, multiple sclerosis, AIDS), and for the  
CC research and development of other therapeutics. This sequence represents  
CC the end of the inserted sequence used to express the peptide display  
CC library (in retroviruses) and used to generate the aptamers of the



CC invention.  
XX Sequence 11 BP; 2 A; 1 C; 2 G; 4 T; 0 U; 2 Other;  
SQ Query Match 30.0%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
|||  
Db 2 GY 4

RESULT 144  
ADJ71749/c  
ID ADJ71749 standard; DNA; 11 BP.  
XX  
AC ADJ71749;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
DE Aptamer peptide display library inserted sequence end.  
XX  
XX cytostatic; analgesic; anticonvulsant; cerebroprotective;  
KW antiparkinsonian; nootropic; neuroprotective; anti-HIV;  
KW modulator of cell phenotype; gene therapy; peptide aptamer;  
KW cell phenotype modification; peptide display library; cancer; pain;  
KW epilepsy; stroke; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; multiple sclerosis; AIDS; ds; Gene; ss.  
XX  
OS Synthetic.  
XX  
XX WO2003040168-A2.  
XX  
XX PD 15-MAY-2003.  
XX  
XX PF 06-NOV-2002; 2002WO-US035584.  
XX  
XX PR 06-NOV-2001; 2001US-0333262P.  
XX  
XX PR 14-FEB-2002; 2002US-0357278P.  
XX  
XX PA (ENAN-) ENANTA PHARM INC.  
XX  
XX Benson JD, Vincent SM, Brasher BB, Miao Z, Lamming D;  
PI WPI; 2003-541418/51.  
XX  
XX DR Identifying peptide aptamer capable of modifying cell phenotype, by  
PT contacting cell sample with library encoding random peptide aptamers,  
PT selecting cell with altered phenotype, and identifying aptamers expressed  
PT in cell.  
XX  
XX Example 1; SEQ ID NO 5; 173pp; English.

CC The invention relates to a method of identifying (M1) a peptide aptamer  
CC (PA) capable of modifying a cell phenotype, involving contacting a 1st  
CC sample of cells with a library of expressible nucleic acid sequences  
CC encoding random peptide aptamers linked to a fusion moiety, selecting at  
CC least one cell having an altered phenotype compared to the phenotype of  
CC the cell prior to contacting, and identifying peptide aptamers expressed  
CC in the selected cell. PA, its derivative or corresponding nucleic acid is  
CC useful for the molecular modelling of an agent having similar binding  
CC characteristics as PA. PA, its derivative or corresponding expressible  
CC nucleic acid is useful for treating or inhibiting a disease or condition  
CC (such as cancer) associated with an aberrant cell phenotype in a subject,  
CC where the aberrant cell phenotype is associated with a change in levels  
CC of apoptosis, viral resistance, signal transduction, protein trafficking,  
CC cell adhesion, membrane transport, cell motility, metabolic state or  
CC differentiation, when compared to a control cell, or the aberrant cell  
CC phenotype is associated with a tumor cell. The expressible nucleic acid  
CC is administered using a retrovirus that comprises a chromatin insulator  
CC element. PA is useful as a prognostic or diagnostic tool, for altering a  
CC cell phenotype, in gene therapy, as therapeutics for treating diseases

CC (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's  
CC disease, Huntington's disease, multiple sclerosis, AIDS), and for the  
CC research and development of other therapeutics. This sequence represents  
CC the end of the inserted sequence used to express the peptide display  
CC library (in retroviruses) and used to generate the aptamers of the  
CC invention.  
XX  
SQ Sequence 11 BP; 2 A; 1 C; 2 G; 4 T; 0 U; 2 Other;  
Query Match 30.0%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 4 RRC 2

RESULT 145  
AAT04535  
ID AAT04535 standard; DNA; 12 BP.  
XX  
AC AAT04535;  
XX  
XX 25-MAR-2003 (revised)  
DT 07-DEC-1995 (first entry)  
XX  
DE Oxygen dependent repressor element.  
XX  
KW Oxygen dependent repressor; ODR; cytotoxic; hypoxic cell; ROX-1;  
KW Tumour Necrosis Factor; TNF; SV-40; mammalian tumour cell; ss.  
XX  
XX Saccharomyces cerevisiae.  
XX  
XX WO9510273-A1.  
XX  
XX PD 20-APR-1995.  
XX  
XX PF 14-OCT-1994; 94WO-US011653.  
XX  
XX PR 14-OCT-1993; 93US-00137238.  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX Giaccia AJ, Koong AC;  
XX  
XX WPI; 1995-161549/21.  
XX  
XX Use of cpds. that activate protein kinase C activity - in hypoxic tumour  
PT cells to mfr. a medicament for killing tumour cells.  
PT  
XX Disclosure; Fig 6a; 4pp; English.

CC This sequence represents an oxygen dependent repressor (ODR) element.  
CC This sequence is specifically bound by the repressor ROX-1. The sequence  
CC is suitable for inclusion in a vector construct that is useful in the  
CC invention. In this vector the ODR element is under the control of an SV-  
CC 40 promoter. This vector induces (under the right conditions) synthesis  
CC of a cytotoxic peptide product. The cytotoxic peptide product is tumour  
CC Necrosis Factor (TNF). The advantage of this vector is that it provides a  
CC more versatile approach to selective killing of regions of hypoxic cells  
CC in solid tumour than hyperthermic treatment of cells. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
XX Sequence 12 BP; 1 A; 2 C; 1 G; 5 T; 0 U; 3 Other;  
SQ Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 146  
AAT04535/c  
ID AAT04535 standard; DNA; 12 BP.  
XX  
AC AAT04535;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-DEC-1995 (first entry)  
XX  
DE Oxygen dependent repressor element.  
XX  
KW Oxygen dependent repressor; ODR; cytotoxic; hypoxic cell; ROX-1;  
KW Tumour Necrosis Factor; TNF; SV-40; mammalian tumour cell; ss.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN W09510273-A1.  
XX  
PD 20-APR-1995.  
XX  
PF 14-OCT-1994; 94WO-US011653.  
XX  
PR 14-OCT-1993; 93US-00137238.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Giaccia AJ, Koong AC;  
XX WPI; 1995-161549/21.  
XX  
DR Use of cpds. that activate protein kinase C activity - in hypoxic tumour  
PT cells to mfr. a medicament for killing tumour cells.  
PT Disclosure; Fig 6a; 44pp; English.  
XX  
PS This sequence represents an oxygen dependent repressor (ODR) element.  
XX This sequence is specifically bound by the repressor ROX-1. The sequence  
CC is suitable for inclusion in a vector construct that is useful in the  
CC invention. In this vector the ODR element is under the control of an SV-  
CC 40 promoter. This vector induces (under the right conditions) synthesis  
CC of a cytotoxic peptide product. The cytotoxic peptide product is tumour  
CC Necrosis Factor (TNF). The advantage of this vector is that it provides a  
CC more versatile approach to selective killing of regions of hypoxic cells  
CC in solid tumour than hyperthermic treatment of cells. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 12 BP; 1 A; 2 C; 1 G; 5 T; 0 U; 3 Other;  
Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
Db 3 RRR 1  
XX  
RESULT 147  
AAT96066  
ID AAT96066 standard; DNA; 12 BP.  
XX  
AC AAT96066;  
XX  
DT 31-MAR-1998 (first entry)  
XX  
DE Recombination region homologous to SINE flanking region.  
XX  
KW Recombination region; consensus defined flanking region;  
KW short interspersed repeated DNA element; SINE; ss.  
XX  
OS Synthetic.

XX US5695977-A.  
PN  
XX 09-DEC-1997.  
PD  
XX 07-MAY-1996; 96US-00643886.  
PF  
XX 31-AUG-1995; 95US-0003063P.  
PR  
XX (GENE-) GENETIC INFORMATION RES INST.  
PA  
XX Jurka JW;  
PI  
XX WPI; 1998-041303/04.  
DR  
XX Genomic integration of DNA by site directed recombination - using  
PT construct containing recombination region homologous to consensus defined  
PT flanking region of short interspersed repeated DNA element.  
XX  
PS Claim 1; Col 11-12; 12pp; English.  
XX  
CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
CC comprises introducing a construct comprising the DNA sequence and a  
CC recombination region homologous to a consensus defined flanking region of  
CC a short interspersed repeated DNA element (SINE), e.g. the present  
CC sequence. The method may be used to modify the phenotype of cells, or  
CC investigate the response of receptors, metabolic pathways or expression  
CC products involved in the regulation of transcription or transduction of  
CC signals. It may also be used to produce protein products and transgenic  
CC animals, by providing novel capabilities to the cells or inhibiting  
CC endogenous capabilities, investigate physiological indications and screen  
CC cosmetics, foods and drugs. By using antisense sequences effective  
CC inhibition of both copies of a gene is possible, ensuring the substantial  
CC absence of the particular transcriptional or translational product. In  
CC addition the method may enhance efficiency in gene therapy, when  
CC providing for a capability in which the host is deficient  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 6 Other;  
Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 YYY 10  
Db 9 YYY 11  
XX  
RESULT 148  
AAT96066/c  
ID AAT96066 standard; DNA; 12 BP.  
XX  
AC AAT96066;  
XX  
DT 31-MAR-1998 (first entry)  
XX  
DE Recombination region homologous to SINE flanking region.  
XX  
KW Recombination region; consensus defined flanking region;  
KW short interspersed repeated DNA element; SINE; ss.  
XX  
OS Synthetic.  
XX  
PN US5695977-A.  
XX  
PD 09-DEC-1997.  
XX  
PF 07-MAY-1996; 96US-00643886.  
XX  
PR 31-AUG-1995; 95US-0003063P.  
XX  
PA (GENE-) GENETIC INFORMATION RES INST.  
XX

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PI Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 1; Col 11-12; 12pp; English.
XX Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX SQ Sequence 12 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db |||
11 RRR 9

RESULT 149
AAT96078
ID AAT96078 standard; DNA; 12 BP.
XX AC AAT96078;
XX 31-MAR-1998 (first entry)
XX DE Recombination region homologous to SINE flanking region.
XX KW Recombination region; consensus defined flanking region;
XX short interspersed repeated DNA element; SINE; ss.
XX OS Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX 07-MAY-1996; 96US-00643886.
XX 31-AUG-1995; 95US-0003063P.
XX (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 7; Col 17-18; 12pp; English.
XX Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX SQ Sequence 12 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db |||
11 RRR 9

RESULT 150
AAT96078/C
ID AAT96078 standard; DNA; 12 BP.
XX AC AAT96078;
XX 31-MAR-1998 (first entry)
XX DE Recombination region homologous to SINE flanking region.
XX KW Recombination region; consensus defined flanking region;
XX short interspersed repeated DNA element; SINE; ss.
XX OS Synthetic.
XX US5695977-A.
XX 09-DEC-1997.
XX 07-MAY-1996; 96US-00643886.
XX 31-AUG-1995; 95US-0003063P.
XX (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
XX WPI; 1998-041303/04.
XX Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX Claim 7; Col 17-18; 12pp; English.
XX Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial

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CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient

XX  
 SQ Sequence 12 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
 |||  
 Db 11 YYY 9

RESULT 151  
 ADG88255  
 ID ADG88255 standard; DNA; 12 BP.  
 XX  
 AC ADG88255;  
 XX  
 XX 22-APR-2004 (first entry)  
 XX Pathogen infection-related gene consensus motif 1 cis element #697.  
 DE  
 KW Pathogen infection-related gene; plant; Peronospora parasitica;  
 KW defence mechanism; pathogen resistance; transgenic plant; oomycete;  
 KW fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;  
 KW motif 1; ds.  
 XX Arabidopsis thaliana.  
 OS  
 XX WO200222675-A2.  
 XX  
 XX 21-MAR-2002.  
 XX  
 XX 14-SEP-2001; 2001WO-US028506.  
 XX  
 XX 15-SEP-2000; 2000US-0232778P.  
 XX  
 XX 22-JUN-2001; 2001US-0300183P.  
 XX  
 XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (WANG/) WANG X.  
 PA (DANG/) DANG J L.  
 PA (EULG/) EULGEM T.  
 PA (ZHUT/) ZHU T.  
 XX  
 PI Glazebrook J, Wang X, Dangl JL, Eulgem T, Zhu T;  
 XX WPI; 2002-292409/33.  
 XX  
 XX Novel isolated polynucleotide, useful for conveying pathogen resistance  
 XX to plants, and for identifying plants infected with a pathogen.  
 XX  
 XX Claim 44; SEQ ID NO 697; 605pp; English.  
 XX  
 XX The invention relates to 691 Arabidopsis thaliana genes (ADG87559--  
 CC ADG87557) whose expression is altered in response to pathogen infection,  
 CC and to homologues of these genes from other plants or fungi, especially  
 CC from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),  
 CC cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The  
 CC expression of genes of the invention was upregulated or downregulated in  
 CC Arabidopsis plants infected with the oomycete Peronospora parasitica  
 CC indicating that they play a role in defence mechanisms. The genes of the  
 CC invention are regulated by RPP7 or RPP8 which act via unconventional  
 CC signalling cascades, or by the RPP4-dependent pathway. The invention also  
 CC relates to polypeptides encoded by the pathogen infection-related genes;  
 CC promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)  
 CC ; expression cassettes, host cells and pathogen-resistant transgenic  
 CC plants and their progeny comprising a polynucleotide of the invention;  
 CC and a method of identifying a plant cell infected with a pathogen. The

CC polynucleotide sequences and methods of the invention are useful for  
 CC identifying plants infected with a pathogen, and for conferring  
 CC resistance to pathogens such as oomycetes, fungi, bacteria, viruses,  
 CC nematodes and insects (e.g., aphids). The present sequence represents a  
 CC consensus sequence for cis elements from the promoters of Arabidopsis  
 CC thaliana genes whose expression is altered in the promoters of Arabidopsis  
 CC parasitica infection. Note: the sequence data for this patent can also be  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 12 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6  
 |||  
 Db 6 CWW 8

RESULT 152  
 ADG88255/C  
 ID ADG88255 standard; DNA; 12 BP.  
 XX  
 AC ADG88255;  
 XX  
 XX 22-APR-2004 (first entry)  
 XX Pathogen infection-related gene consensus motif 1 cis element #697.  
 DE  
 KW Pathogen infection-related gene; plant; Peronospora parasitica;  
 KW defence mechanism; pathogen resistance; transgenic plant; oomycete;  
 KW fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;  
 KW motif 1; ds.  
 XX Arabidopsis thaliana.  
 OS  
 XX WO200222675-A2.  
 XX  
 XX 21-MAR-2002.  
 XX  
 XX 14-SEP-2001; 2001WO-US028506.  
 XX  
 XX 15-SEP-2000; 2000US-0232778P.  
 XX  
 XX 22-JUN-2001; 2001US-0300183P.  
 XX  
 XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (WANG/) WANG X.  
 PA (DANG/) DANG J L.  
 PA (EULG/) EULGEM T.  
 PA (ZHUT/) ZHU T.  
 XX  
 PI Glazebrook J, Wang X, Dangl JL, Eulgem T, Zhu T;  
 XX WPI; 2002-292409/33.  
 XX  
 XX Novel isolated polynucleotide, useful for conveying pathogen resistance  
 XX to plants, and for identifying plants infected with a pathogen.  
 XX  
 XX Claim 44; SEQ ID NO 697; 605pp; English.  
 XX  
 XX The invention relates to 691 Arabidopsis thaliana genes (ADG87559--  
 CC ADG87557) whose expression is altered in response to pathogen infection,  
 CC and to homologues of these genes from other plants or fungi, especially  
 CC from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),  
 CC cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The  
 CC expression of genes of the invention was upregulated or downregulated in  
 CC Arabidopsis plants infected with the oomycete Peronospora parasitica,  
 CC indicating that they play a role in defence mechanisms. The genes of the  
 CC invention are regulated by RPP7 or RPP8 which act via unconventional

CC signalling cascades, or by the RPP4-dependent pathway. The invention also  
 CC relates to polypeptides encoded by the pathogen infection-related genes;  
 CC promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)  
 CC ; expression cassettes, host cells and pathogen-resistant transgenic  
 CC plants and their progeny comprising a polynucleotide of the invention;  
 CC and a method of identifying a plant cell infected with a pathogen. The  
 CC polynucleotide sequences and methods of the invention are useful for  
 CC identifying plants infected with a pathogen, and for conferring  
 CC resistance to pathogens such as oomycetes, fungi, bacteria, viruses,  
 CC nematodes and insects (e.g., aphids). The present sequence represents a  
 CC consensus sequence for cis elements from the promoters of Arabidopsis  
 CC thaliana genes whose expression is altered in response to Peronospora  
 CC parvatica infection. Note: The sequence data for this patent can also be  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 12 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7  
 |||  
 Db 8 WWG 6

#### RESULT 153

ADB81333  
 ID ADB81333 standard; DNA; 12 BP.

AC ADB81333;

DT 04-DEC-2003 (first entry)

XX Bacteriophage phi-C31 consensus splice acceptor site (SeqID 3).

XX splice acceptor site; ss; phiC31 integrase; C31-Int;

KW site specific recombinase; SSR; gene function; disease model;

KW gene therapy; transgenic.

XX Bacteriophage phi-C31.

OS WO2003066867-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-EP001122.

XX 06-FEB-2002; 2002US-0354741P.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX Andreas S, Faust N;

XX WPI; 2003-663599/62.

XX New genetically engineered nucleic acid molecule, useful for preparing an  
 PT agent for recombining a DNA molecule containing phiC31 integrase  
 PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic  
 PT organism.

PS Claim 10; Page 40; 87pp; English.

XX This invention relates to novel genetically engineered nucleic acid  
 CC molecules encoding phiC31 integrase (C31-Int), which has been codon  
 CC optimised for expression in eukaryotic host cells. The phiC31 integrase  
 CC is a site specific recombinase (SSR) that catalyzes recombination between  
 CC two phiC31 recognition sequences. The introduction of silent mutations  
 CC into the coding sequence changes the given codon to one that is most  
 CC frequently used in the respective host, which in turn alters expression  
 CC levels. Accordingly, using this ability to generate controlled and  
 CC permanent modifications in eukaryotic genomes has various research

CC applications including the study of gene function and the creation of  
 CC disease models, as well as gene therapy for medical applications, and the  
 CC design of economically important animals and crops. Furthermore, the  
 CC phiC31 integrase of the invention is useful for preparing an agent for  
 CC recombining a DNA molecule containing phiC31 integrase recognition  
 CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This  
 CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus  
 CC splice acceptor site (SeqID 3) of the invention.

XX Sequence 12 BP; 1 A; 1 C; 2 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 10; Length 12;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
 |||  
 Db 1 YYY 3

#### RESULT 154

ADB81333/c  
 ID ADB81333 standard; DNA; 12 BP.

XX AC ADB81333;

XX 04-DEC-2003 (first entry)

XX Bacteriophage phi-C31 consensus splice acceptor site (SeqID 3).

XX splice acceptor site; ss; phiC31 integrase; C31-Int;

KW site specific recombinase; SSR; gene function; disease model;

KW gene therapy; transgenic.

XX Bacteriophage phi-C31.

XX WO2003066867-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-EP001122.

XX 06-FEB-2002; 2002US-0354741P.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX Andreas S, Faust N;

XX WPI; 2003-663599/62.

XX New genetically engineered nucleic acid molecule, useful for preparing an  
 PT agent for recombining a DNA molecule containing phiC31 integrase  
 PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic  
 PT organism.

PS Claim 10; Page 40; 87pp; English.

XX This invention relates to novel genetically engineered nucleic acid  
 CC molecules encoding phiC31 integrase (C31-Int), which has been codon  
 CC optimised for expression in eukaryotic host cells. The phiC31 integrase  
 CC is a site specific recombinase (SSR) that catalyzes recombination between  
 CC two phiC31 recognition sequences. The introduction of silent mutations  
 CC into the coding sequence changes the given codon to one that is most  
 CC frequently used in the respective host, which in turn alters expression  
 CC levels. Accordingly, using this ability to generate controlled and  
 CC permanent modifications in eukaryotic genomes has various research  
 CC applications including the study of gene function and the creation of  
 CC disease models, as well as gene therapy for medical applications, and the  
 CC design of economically important animals and crops. Furthermore, the  
 CC phiC31 integrase of the invention is useful for preparing an agent for  
 CC recombining a DNA molecule containing phiC31 integrase recognition  
 CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This  
 CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus

```
CC splice acceptor site (SeqID 3) of the invention.
XX
SQ Sequence 12 BP; 1 A; 1 C; 2 G; 0 T; 0 U; 8 Other;

Query Match      30.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 7 RRR 5

RESULT 155
ADB81334
ID ADB81334 standard; DNA; 12 BP.
XX
AC ADB81334;
XX
DT 04-DEC-2003 (first entry)
DE Bacteriophage phi-C31 consensus splice acceptor site (SeqID 4).
XX
KW splice acceptor site; ss; phiC31 integrase; C31-Int;
KW site specific recombinase; SSR; gene function; disease model;
KW gene therapy; transgenic.
XX
OS Bacteriophage phi-C31.
XX
PN WO2003066867-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001122.
XX
PR 06-FEB-2002; 2002US-0354741P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Andreas S, Faust N;
XX
PS WPI; 2003-663599/62.
XX
PT New genetically engineered nucleic acid molecule, useful for preparing an
PT agent for recombining a DNA molecule containing phiC31 integrase
PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT organism.
XX
PS Claim 10; Page 40; 87pp; English.
XX
CC This invention relates to novel genetically engineered nucleic acid
CC molecules encoding phiC31 integrase (C31-Int), which has been codon
CC optimised for expression in eukaryotic host cells. The phiC31 integrase
CC is a site specific recombinase (SSR) that catalyzes recombination between
CC two phiC31 recognition sequences. The introduction of silent mutations
CC into the coding sequence changes the given codon to one that is most
CC frequently used in the respective host, which in turn alters expression
CC levels. Accordingly, using this ability to generate controlled and
CC permanent modifications in eukaryotic genomes has various research
CC applications including the study of gene function and the creation of
CC disease models, as well as gene therapy for medical applications, and the
CC design of economically important animals and crops. Furthermore, the
CC phiC31 integrase of the invention is useful for preparing an agent for
CC recombining a DNA molecule containing phiC31 integrase recognition
CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus
CC splice acceptor site (SeqID 4) of the invention.
XX
SQ Sequence 12 BP; 1 A; 0 C; 2 G; 1 T; 0 U; 8 Other;

Query Match      30.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 7 RRR 5

RESULT 157
ADB81334
ID ADB81334 standard; DNA; 12 BP.
XX
AC ADB81334;
XX
DT 04-DEC-2003 (first entry)
DE Bacteriophage phi-C31 consensus splice acceptor site (SeqID 4).
XX
KW splice acceptor site; ss; phiC31 integrase; C31-Int;
KW site specific recombinase; SSR; gene function; disease model;
KW gene therapy; transgenic.
XX
OS Bacteriophage phi-C31.
XX
PN WO2003066867-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001122.
XX
PR 06-FEB-2002; 2002US-0354741P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Andreas S, Faust N;
XX
PS WPI; 2003-663599/62.
XX
PT New genetically engineered nucleic acid molecule, useful for preparing an
PT agent for recombining a DNA molecule containing phiC31 integrase
PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT organism.
XX
PS Claim 10; Page 40; 87pp; English.
XX
CC This invention relates to novel genetically engineered nucleic acid
CC molecules encoding phiC31 integrase (C31-Int), which has been codon
CC optimised for expression in eukaryotic host cells. The phiC31 integrase
CC is a site specific recombinase (SSR) that catalyzes recombination between
CC two phiC31 recognition sequences. The introduction of silent mutations
CC into the coding sequence changes the given codon to one that is most
CC frequently used in the respective host, which in turn alters expression
CC levels. Accordingly, using this ability to generate controlled and
CC permanent modifications in eukaryotic genomes has various research
CC applications including the study of gene function and the creation of
CC disease models, as well as gene therapy for medical applications, and the
CC phiC31 integrase of the invention is useful for preparing an agent for
CC recombining a DNA molecule containing phiC31 integrase recognition
CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus
CC splice acceptor site (SeqID 4) of the invention.
XX
SQ Sequence 12 BP; 1 A; 0 C; 2 G; 1 T; 0 U; 8 Other;
```

```

AAT96067
ID AAT96067 standard; DNA; 13 BP.
XX
AC AAT96067;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
   |||
Db 10 YY 12

RESULT 158
AAT96067/c
ID AAT96067 standard; DNA; 13 BP.
XX
AC AAT96067;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.

```

```

XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
   |||
Db 12 RRR 10

RESULT 159
AAT96079
ID AAT96079 standard; DNA; 13 BP.
XX
AC AAT96079;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX

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PA (GENE-) GENETIC INFORMATION RES INST.
XX Jurka JW;
PI
XX
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
XX Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
DB 10 RRR 12

RESULT 160
AAT96079/c
ID AAT96079 standard; DNA; 13 BP.
XX
XX
AC AAT96079;
XX
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
XX US5695977-A.
PN
XX
XX 09-DEC-1997.
PD
XX
XX 07-MAY-1996; 96US-00643886.
PF
XX
XX 31-AUG-1995; 95US-0003063P.
PR
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
XX Jurka JW;
PI
XX
XX WPI; 1998-041303/04.
DR
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
XX Claim 7; Col 17-18; 12pp; English.
PS

XX Integrating a DNA sequence into the genome of a vertebrate host cell,
XX comprises introducing a construct comprising the DNA sequence and a
XX recombination region homologous to a consensus defined flanking region of
XX a short interspersed repeated DNA element (SINE), e.g. the present
XX sequence. The method may be used to modify the phenotype of cells, or
XX investigate the response of receptors, metabolic pathways or expression
XX products involved in the regulation of transcription or transduction of
XX signals. It may also be used to produce protein products and transgenic
XX animals, by providing novel capabilities to the cells or inhibiting
XX endogenous capabilities, investigate physiological indications and screen
XX cosmetics, foods and drugs. By using antisense sequences effective
XX inhibition of both copies of a gene is possible, ensuring the substantial
XX absence of the particular transcriptional or translational product. In
XX addition the method may enhance efficiency in gene therapy, when
XX providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
DB 12 YYY 10

RESULT 161
ABL42250
ID ABL42250 standard; DNA; 13 BP.
XX
XX
AC ABL42250;
XX
XX
DT 29-AUG-2003 (revised)
DT 01-JUL-2002 (first entry)
XX
XX
DE Animal cis-regulatory sequence from MBF-1.
XX
KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;
KW gene family; ds.
XX
XX Metazoa.
OS
XX
XX WO200162967-A2.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 19-FEB-2001; 2001WO-1L000151.
PF
XX
XX 22-FEB-2000; 2000IL-00134660.
PR
XX
XX 02-JUL-2000; 2000IL-00137124.
PR
XX
XX 20-AUG-2000; 2000IL-00137959.
PR
XX
XX (GENE-) GENENA LTD.
PA
XX
XX (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
PA
XX
XX Vider B, Katzir N;
PI
XX
XX WPI; 2002-239525/29.
DR
XX
XX Polymerase chain reaction based method of DNA fingerprinting, useful for
XX analyzing genes, e.g. for identifying genes involved in cancer formation,
XX involves using a mix of primers that match the conserved regions of a
XX gene family.
XX
XX Example; Page 16; 28pp; English.
PS
XX
XX The invention relates to a polymerase chain reaction (PCR) based method
XX of DNA fingerprinting, comprising using primers that match the conserved
XX regions of a gene family. The method is useful for gene expression
XX analysis of any cell or tissue, or for the performance of DNA
XX fingerprinting analysis of the same organism in order that one will

```



CC reveal the function of a gene that produced differential product between  
 CC genotypes. The method is also useful for identifying PCR reactions that  
 CC contain a gene of interest in a gene family reverse transcriptase (RT)-  
 CC PCR expression analysis. The method is also useful for identifying genes  
 CC that belong to a gene family that might be involved in cancer formation.  
 CC The method is particularly useful for comparing genomic sequences. These  
 CC are also applicable in agriculture (e.g. to mark useful genes to assist  
 CC breeding). The current sequence represents an animal cis-regulatory  
 CC sequence. This is used in DNA fingerprinting using primers or a mix of  
 CC primers that match the sequence of ubiquitous cis-acting regulatory  
 CC elements. (Updated on 29-AUG-2003 to standardise OS field)  
 SQ Sequence 13 BP; 7 A; 0 C; 0 G; 2 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
 |||  
 Db 11 YYY 13

RESULT 162  
 ABL42250/c  
 ID ABL42250 standard; DNA; 13 BP.

AC ABL42250;

DT 29-AUG-2003 (revised)  
 DT 01-JUL-2002 (first entry)

XX Animal cis-regulatory sequence from MBF-1.

KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;  
 KW gene family; ds.

XX Metazoa.

XX WO200162967-A2.

XX 30-AUG-2001.

XX 19-FEB-2001; 2001WO-IL000151.

XX 22-FEB-2000; 2000IL-00134660.

XX 02-JUL-2000; 2000IL-00137124.

XX 20-AUG-2000; 2000IL-00137959.

XX (GENE-) GENENA LTD.

PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.

XX Vider B, Katzir N;

XX WPI; 2002-239525/29.

XX Polymerase chain reaction based method of DNA fingerprinting, useful for  
 PT analyzing genes, e.g. for identifying genes involved in cancer formation,  
 PT involves using a mix of primers that match the conserved regions of a  
 PT gene family.

PS Example; Page 16; 28pp; English.

XX The invention relates to a polymerase chain reaction (PCR) based method  
 CC of DNA fingerprinting, comprising using primers that match the conserved  
 CC regions of a gene family. The method is useful for gene expression  
 CC analysis of any cell or tissue, or for the performance of DNA  
 CC fingerprinting analysis of the same organism in order that one will  
 CC reveal the function of a gene that produced differential product between  
 CC genotypes. The method is also useful for identifying PCR reactions that  
 CC contain a gene of interest in a gene family reverse transcriptase (RT)-  
 CC PCR expression analysis. The method is also useful for identifying genes  
 CC that belong to a gene family that might be involved in cancer formation.

CC The method is particularly useful for comparing genomic sequences. These  
 CC are also applicable in agriculture (e.g. to mark useful genes to assist  
 CC breeding). The current sequence represents an animal cis-regulatory  
 CC sequence. This is used in DNA fingerprinting using primers or a mix of  
 CC primers that match the sequence of ubiquitous cis-acting regulatory  
 CC elements. (Updated on 29-AUG-2003 to standardise OS field)  
 SQ Sequence 13 BP; 7 A; 0 C; 0 G; 2 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
 |||  
 Db 13 RRR 11

RESULT 163  
 ADL71828  
 ID ADL71828 standard; DNA; 13 BP.

AC ADL71828;

DT 20-MAY-2004 (first entry)

XX Anticancer agent-related Y-box DNA sequence.

XX anticancer agent; cancer; decoy oligonucleotide; transcriptional factor;  
 KW YB-1 gene; ds; Y-box.

XX Unidentified.

XX KR2002025421-A.

XX 04-APR-2002.

XX 29-SEP-2000; 2000KR-00057192.

XX 29-SEP-2000; 2000KR-00057192.

XX (AHNB/) AHN B W.

XX (HANS/) HAN S W.

XX (KIMK/) KIM K K.

XX (KIMS/) KIM S J.

XX (SHIN/) SHIN B A.

XX Ahn BW, Han SW, Jung SS, Kim KK, Kim SJ, Kim YR, Shin BA;

XX WPI; 2003-500926/47.

XX Composition of anticancer agent containing decoy oligonucleotides binding  
 PT to transcriptional factors of yb-1 gene.

XX Disclosure; Page 3; 9pp; Korean.

XX The invention comprises an anticancer agent containing decoy  
 CC oligonucleotides which bind to transcriptional factors of the YB-1 gene.  
 CC The decoy oligonucleotides selectively suppress the growth of cancer  
 CC cells without affecting normal cells. The present DNA sequence was used  
 CC in the exemplification of the invention.

XX Sequence 13 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 9  
 |||  
 Db 9 GYY 11

RESULT 164  
ADL71828/c  
ID ADL71828 standard; DNA; 13 BP.  
XX  
AC ADL71828;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Anticancer agent-related Y-box DNA sequence.  
XX  
KW anticancer agent; cancer; decoy oligonucleotide; transcriptional factor;  
XX YB-1 gene; ds, Y-box.  
XX  
OS Unidentified.  
XX  
FN KR2002025421-A.  
XX  
PD 04-APR-2002.  
XX  
PF 29-SEP-2000; 2000KR-00057192.  
XX  
PR 29-SEP-2000; 2000KR-00057192.  
XX  
PA (AHNB/) AHN B W.  
PA (HANS/) HAN S W.  
PA (KIMK/) KIM K K.  
PA (KIMS/) KIM S J.  
PA (SHIN/) SHIN B A.  
XX  
PI Ahn BW, Han SW, Jung SS, Kim KK, Kim SJ, Kim YR, Shin BA;  
XX  
DR WPI; 2003-500926/47.  
XX  
PT Composition of anticancer agent containing decoy oligonucleotides binding  
PT to transcriptional factors of yb-1 gene.  
XX  
PS Disclosure; Page 3; 9pp; Korean.  
XX  
CC The invention comprises an anticancer agent containing decoy  
CC oligonucleotides which bind to transcriptional factors of the YB-1 gene.  
CC The decoy oligonucleotides selectively suppress the growth of cancer  
CC cells without affecting normal cells. The present DNA sequence was used  
CC in the exemplification of the invention.  
XX  
SQ Sequence 13 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 2 Other;  
  
Query Match 30.0%; Score 3; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 RRC 4  
DB 11 RRC 9  
  
RESULT 165  
ACC85667  
ID ACC85667 standard; DNA; 13 BP.  
XX  
AC ACC85667;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE RNA ligand aptamer marker/probe NCW13.  
XX  
KW RNA aptamer; ligand; heat shock factor protein; PCR; primer; ss.  
XX Synthetic.  
XX  
FN WO2004001065-A2.  
XX  
PD 31-DEC-2003.  
XX  
PS Example 1; Page 64; Opp; English.  
XX  
CC The present invention relates to a method of identifying RNA ligands that

PF 24-JUN-2003; 2003WO-US019966.  
XX  
PR 24-JUN-2002; 2002US-0391255P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Shi H, Lis JT;  
XX  
DR WPI; 2004-071741/07.  
XX  
PT Identifying RNA ligands that bind to a target molecule comprises treating  
PT a first pool of RNA ligands that collectively bind more than one target  
PT to reduce the concentration or eliminate the presence of target-binding  
PT RNA ligands.  
XX  
PS Example 1; Page 64; Opp; English.  
XX  
CC The present invention relates to a method of identifying RNA ligands that  
CC bind to a target molecule, comprising treating a first pool of RNA  
CC ligands that collectively bind more than one target under conditions  
CC effective to reduce the concentration or eliminate the presence of one or  
CC more predominate target-binding RNA ligands from the first pool of RNA  
CC ligands. In particular, the method can be used to identify RNA aptamers  
CC capable of binding to heat shock factor protein. The present sequence is  
CC a DNA sequence shown in the exemplification of the invention  
XX  
SQ Sequence 13 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 7 Other;  
  
Query Match 30.0%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CWV 6  
DB 5 CWV 7  
  
RESULT 166  
ACC85667/c  
ID ACC85667 standard; DNA; 13 BP.  
XX  
AC ACC85667;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE RNA ligand aptamer marker/probe NCW13.  
XX  
KW RNA aptamer; ligand; heat shock factor protein; PCR; primer; ss.  
XX Synthetic.  
XX  
FN WO2004001065-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 24-JUN-2003; 2003WO-US019966.  
XX  
PR 24-JUN-2002; 2002US-0391255P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Shi H, Lis JT;  
XX  
DR WPI; 2004-071741/07.  
XX  
PT Identifying RNA ligands that bind to a target molecule comprises treating  
PT a first pool of RNA ligands that collectively bind more than one target  
PT to reduce the concentration or eliminate the presence of target-binding  
PT RNA ligands.  
XX  
PS Example 1; Page 64; Opp; English.  
XX  
CC The present invention relates to a method of identifying RNA ligands that

CC bind to a target molecule, comprising treating a first pool of RNA  
 CC ligands that collectively bind more than one target under conditions  
 CC effective to reduce the concentration or eliminate the presence of one or  
 CC more predominate target-binding RNA ligands from the first pool of RNA  
 CC ligands. In particular, the method can be used to identify RNA aptamers  
 CC capable of binding to heat shock factor protein. The present sequence is  
 CC a DNA sequence shown in the exemplification of the invention  
 XX  
 SQ Sequence 13 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WVG 7  
 ||||  
 Db 7 WVG 5

RESULT 167  
 AAQ80951  
 ID AAQ80951 standard; RNA; 14 BP.  
 XX  
 AC AAQ80951;  
 XX  
 DT 27-FEB-1996 (first entry)  
 XX  
 DE HIV protease inhibitory oligoribonucleotide sequence (d).  
 XX  
 KW Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;  
 KW diagnostic probe; ss.  
 XX  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FT misc\_difference 1..14  
 FT /\*tag= a  
 FT /note= "each nucleotide is opt. modified"

PN WO9429479-A1.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 09-JUN-1994; 94WO-US006456.  
 XX  
 PR 09-JUN-1993; 93US-00073873.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.

Beutel BA, Sherman MI, Coppola GR;  
 WPI; 1995-036501/05.

Inhibiting HIV protease function with specific oligonucleotides - which  
 bind to the enzyme, for treating or preventing HIV infection, including  
 use of vectors in gene therapy.

Claim 4; Page 51; 81pp; English.

HIV protease function is inhibited by RNA oligonucleotides which include  
 one of the sequences 5'-AANGU, 5'-ANUGGA, 5'-AGUGUG, 5'-UNGAUNY, 5'-CCUC,  
 5'-GGUGNA or one of the sequences in AAQ80950- AAQ80953. Oligonucleotides  
 contg. these sequences are found to bind to HIV protease and so prevent  
 HIV maturation. Pred. oligoribonucleotides are classified into classes A  
 (AAQ80954-Q80964), B (AAQ80965-Q80967) and C (AAQ80968-Q80972) and can be  
 single- or double- stranded or in the form of a stem-loop structure, a  
 pseudoknot or a closed, circular structure. In addition to their  
 potential use in gene therapy, the oligonucleotides will be useful as  
 diagnostic probes to detect HIV infection

Sequence 14 BP; 4 A; 1 C; 5 G; 0 T; 1 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRR 3  
 ||||  
 Db 12 RRR 14

RESULT 168  
 AAQ80951/C  
 ID AAQ80951 standard; RNA; 14 BP.  
 XX  
 AC AAQ80951;  
 XX  
 DT 27-FEB-1996 (first entry)  
 XX  
 DE HIV protease inhibitory oligoribonucleotide sequence (d).  
 XX  
 KW Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;  
 KW diagnostic probe; ss.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 FT misc\_difference 1..14  
 FT /\*tag= a  
 FT /note= "each nucleotide is opt. modified"

PN WO9429479-A1.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 09-JUN-1994; 94WO-US006456.  
 XX  
 PR 09-JUN-1993; 93US-00073873.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Sherman MI, Coppola GR;  
 XX  
 DR WPI; 1995-036501/05.

Inhibiting HIV protease function with specific oligonucleotides - which  
 bind to the enzyme, for treating or preventing HIV infection, including  
 use of vectors in gene therapy.

Claim 4; Page 51; 81pp; English.

HIV protease function is inhibited by RNA oligonucleotides which include  
 one of the sequences 5'-AANGU, 5'-ANUGGA, 5'-AGUGUG, 5'-UNGAUNY, 5'-CCUC,  
 5'-GGUGNA or one of the sequences in AAQ80950- AAQ80953. Oligonucleotides  
 contg. these sequences are found to bind to HIV protease and so prevent  
 HIV maturation. Pred. oligoribonucleotides are classified into classes A  
 (AAQ80954-Q80964), B (AAQ80965-Q80967) and C (AAQ80968-Q80972) and can be  
 single- or double- stranded or in the form of a stem-loop structure, a  
 pseudoknot or a closed, circular structure. In addition to their  
 potential use in gene therapy, the oligonucleotides will be useful as  
 diagnostic probes to detect HIV infection

Sequence 14 BP; 4 A; 1 C; 5 G; 0 T; 1 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
 ||||  
 Db 14 YYY 12

RESULT 169  
 AAQ80974  
 ID AAQ80974 standard; DNA; 14 BP.

```

XX AC AAQ80974;
XX AC
XX DT 27-FEB-1996 (first entry)
XX DT
XX DE HIV protease inhibitory oligodeoxyribonucleotide sequence (n).
XX DE
XX KW Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
XX KW diagnostic probe; ss.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT misc_difference 1..14
XX FT /*tag= a
XX FT /note= "each nucleotide is opt. modified"
XX FT
XX PN WO9429479-A1.
XX PN
XX PD 22-DEC-1994.
XX PD
XX PF 09-JUN-1994; 94WO-US006456.
XX PF
XX PR 09-JUN-1993; 93US-00073873.
XX PR
XX PR (PHAR-) PHARMAGENICS INC.
XX PA
XX PI Beutel BA, Sherman MI, Coppola GR;
XX PI WPI; 1995-036501/05.
XX DR
XX DR
XX FT Inhibiting HIV protease function with specific oligonucleotides - which
XX FT bind to the enzyme, for treating or preventing HIV infection, including
XX FT use of vectors in gene therapy.
XX PS
XX PS Claim 12; Page 54; 81pp; English.
XX CC
XX CC HIV protease function is inhibited by DNA oligonucleotides which include
XX CC one of the sequences 5'-AANGT, 5'-ANTGGA, 5'-AGTGTG, 5'-TNGATNY, 5'-CCTC,
XX CC 5'-GGTGNA or one of the sequences in AAQ80973- AAQ80976. Oligonucleotides
XX CC contg. these sequences are found to bind to HIV protease and so prevent
XX CC HIV maturation. Prefd. oligo- deoxyribonucleotides are classified into
XX CC classes D (AAQ80977-Q80987), E (AAQ80988-Q80990) and F (AAQ80991-Q80995)
XX CC and can be single- or double- stranded or in the form of a stem-loop
XX CC structure, a pseudoknot or a closed, circular structure. In addition to
XX CC their potential use in gene therapy, the oligonucleotides will be useful
XX CC as diagnostic probes to detect HIV infection
XX SQ
XX SQ Sequence 14 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 3 Other;
XX
XX Query Match 30.0%; Score 3; DB 2; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RRR 3
XX DB 12 RRR 14
XX
XX RESULT 170
XX ID AAQ80974/c
XX AC AAQ80974 standard; DNA; 14 BP.
XX AC
XX AC AAQ80974;
XX DT 27-FEB-1996 (first entry)
XX DT
XX DE HIV protease inhibitory oligodeoxyribonucleotide sequence (n).
XX DE
XX KW Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
XX KW diagnostic probe; ss.
XX OS
XX OS Synthetic.

```

```

XX FH
XX FH Key Location/Qualifiers
XX FT misc_difference 1..14
XX FT /*tag= a
XX FT /note= "each nucleotide is opt. modified"
XX FT
XX PN WO9429479-A1.
XX PN
XX PD 22-DEC-1994.
XX PD
XX PF 09-JUN-1994; 94WO-US006456.
XX PF
XX PR 09-JUN-1993; 93US-00073873.
XX PR
XX PR (PHAR-) PHARMAGENICS INC.
XX PA
XX PI Beutel BA, Sherman MI, Coppola GR;
XX PI WPI; 1995-036501/05.
XX DR
XX DR
XX FT Inhibiting HIV protease function with specific oligonucleotides - which
XX FT bind to the enzyme, for treating or preventing HIV infection, including
XX FT use of vectors in gene therapy.
XX PS
XX PS Claim 12; Page 54; 81pp; English.
XX CC
XX CC HIV protease function is inhibited by DNA oligonucleotides which include
XX CC one of the sequences 5'-AANGT, 5'-ANTGGA, 5'-AGTGTG, 5'-TNGATNY, 5'-CCTC,
XX CC 5'-GGTGNA or one of the sequences in AAQ80973- AAQ80976. Oligonucleotides
XX CC contg. these sequences are found to bind to HIV protease and so prevent
XX CC HIV maturation. Prefd. oligo- deoxyribonucleotides are classified into
XX CC classes D (AAQ80977-Q80987), E (AAQ80988-Q80990) and F (AAQ80991-Q80995)
XX CC and can be single- or double- stranded or in the form of a stem-loop
XX CC structure, a pseudoknot or a closed, circular structure. In addition to
XX CC their potential use in gene therapy, the oligonucleotides will be useful
XX CC as diagnostic probes to detect HIV infection
XX SQ
XX SQ Sequence 14 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 3 Other;
XX
XX Query Match 30.0%; Score 3; DB 2; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 YYY 10
XX DB 14 YYY 12
XX
XX RESULT 171
XX ID AAT96068
XX AC AAT96068 standard; DNA; 14 BP.
XX AC
XX AC AAT96068;
XX DT 31-MAR-1998 (first entry)
XX DT
XX DE Recombination region homologous to SINE flanking region.
XX DE
XX DE Recombination region; consensus defined flanking region;
XX KW short interspersed repeated DNA element; SINE; ss.
XX KW
XX OS Synthetic.
XX OS
XX PN US5695977-A.
XX PN
XX PD 09-DEC-1997.
XX PD
XX PF 07-MAY-1996; 96US-00643886.
XX PF
XX PR 31-AUG-1995; 95US-0003063P.
XX PR
XX PA (GENE-) GENETIC INFORMATION RES INST.
XX PA

```

PI Jurka JW;  
 XX WPI; 1998-041303/04.  
 XX Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 PS Claim 1; Col 13-14; 12pp; English.  
 XX  
 CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient  
 XX  
 SQ Sequence 14 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 8 Other;  
 Query Match 30.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 DB 11 YYY 13  
 RESULT 172  
 AAT96068/c  
 ID AAT96068 standard; DNA; 14 BP.  
 AC AAT96068;  
 XX  
 DT 31-MAR-1998 (first entry)  
 DE Recombination region homologous to SINE flanking region.  
 XX  
 KW Recombination region; consensus defined flanking region;  
 KW short interspersed repeated DNA element; SINE; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US5695977-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 07-MAY-1996; 96US-00643886.  
 XX  
 PR 31-AUG-1995; 95US-0003063P.  
 XX  
 PA (GENE-) GENETIC INFORMATION RES INST.  
 XX  
 PI Jurka JW;  
 XX  
 DR WPI; 1998-041303/04.  
 XX  
 CC Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 PS Claim 1; Col 13-14; 12pp; English.  
 XX  
 CC Integrating a DNA sequence into the genome of a vertebrate host cell,

CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient  
 XX  
 SQ Sequence 14 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 8 Other;  
 Query Match 30.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRR 3  
 DB 13 RRR 11  
 RESULT 173  
 AAT96080  
 ID AAT96080 standard; DNA; 14 BP.  
 XX  
 AC AAT96080;  
 XX  
 DT 31-MAR-1998 (first entry)  
 DE Recombination region homologous to SINE flanking region.  
 XX  
 KW Recombination region; consensus defined flanking region;  
 KW short interspersed repeated DNA element; SINE; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US5695977-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 07-MAY-1996; 96US-00643886.  
 XX  
 PR 31-AUG-1995; 95US-0003063P.  
 XX  
 PA (GENE-) GENETIC INFORMATION RES INST.  
 XX  
 PI Jurka JW;  
 XX  
 DR WPI; 1998-041303/04.  
 XX  
 CC Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 PS Claim 7; Col 17-18; 12pp; English.  
 XX  
 CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial

CC absence of the particular transcriptional or translational product. In  
CC addition the method may enhance efficiency in gene therapy, when  
CC providing for a capability in which the host is deficient

XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 10 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
11 RRR 13

## RESULT 174

AAAT96080/c  
ID AAT96080 standard; DNA; 14 BP.

XX AC AAT96080;

XX DT 31-MAR-1998 (first entry)

XX DE Recombination region homologous to SINE flanking region.

XX KW Recombination region; consensus defined flanking region;  
XX short interspersed repeated DNA element; SINE; ss.

XX OS Synthetic.

XX XX US5695977-A.

XX PD 09-DEC-1997.

XX PF 07-MAY-1996; 96US-00643886.

XX PR 31-AUG-1995; 95US-0003063P.

XX PA (GENE-) GENETIC INFORMATION RES INST.

XX PI JurKa JW;

XX DR WPI; 1998-041303/04.

XX PT Genomic integration of DNA by site directed recombination - using  
XX construct containing recombination region homologous to consensus defined  
XX flanking region of short interspersed repeated DNA element.

XX PS Claim 7; Col 17-18; 12pp; English.

XX CC Integrating a DNA sequence into the genome of a vertebrate host cell,  
XX comprises introducing a construct comprising the DNA sequence and a  
XX recombination region homologous to a consensus defined flanking region of  
XX a short interspersed repeated DNA element (SINE), e.g. the present  
XX sequence. The method may be used to modify the phenotype of cells, or  
XX investigate the response of receptors, metabolic pathways or expression  
XX products involved in the regulation of transcription or transduction of  
XX signals. It may also be used to produce protein products and transgenic  
XX animals, by providing novel capabilities to the cells or inhibiting  
XX endogenous capabilities, investigate physiological indications and screen  
XX cosmetics, foods and drugs. By using antisense sequences effective  
XX inhibition of both copies of a gene is possible, ensuring the substantial  
XX absence of the particular transcriptional or translational product. In  
XX addition the method may enhance efficiency in gene therapy, when  
XX providing for a capability in which the host is deficient

XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 10 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

DB 13 YYY 11

## RESULT 175

AAV22311  
ID AAV22311 standard; cDNA; 14 BP.

XX AC AAV22311;

XX DT 29-JUN-1998 (first entry)

XX DE ISRE gene promoter motif found in a trophoblast STAT utron.

XX KW Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;  
XX interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
XX antigen expression; gene promoter; class I; class II; IFN signalling;  
XX GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;  
XX B7-2; FC gamma R; HIV gene expression; transplant rejection; treatment;  
XX autoimmune disease; inflammatory disease; ss.

XX OS Unidentified.

XX PN WO9744450-A1.

XX PD 27-NOV-1997.

XX PF 21-MAY-1997; 97WO-US009459.

XX PR 21-MAY-1996; 96US-00646789.

XX PA (UYIA ) UNIV YALE.

XX PI Peyman JA;

XX DR WPI; 1998-018505/02.

XX PT Utrons, RNA molecules containing promoter regulatory motifs - useful to  
XX suppress express expression from promoter of interest, specifically TSU  
XX nucleic acid suppression of MHC Class I and II gene expression.

XX PS Disclosure; Page 89; 200pp; English.

XX CC The present sequence represents an ISRE gene promoter motif found in a  
XX trophoblast STAT utron (TSU). TSUs be isolated from a CDNA library  
XX prepared from mRNA isolated from trophoblast cells. Utrons are from, or  
XX are homologous to, the 3' untranslated region (UTR), of an mRNA that  
XX stimulates or inhibits a cellular response by sequence specific  
XX interactions. The TSU is able to suppress constitutive and interferon-  
XX gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I  
XX and class II antigen expression and expression of other antigens, the  
XX gene promoters of which contain related sequence motifs that are  
XX stimulated by the same factors which stimulate MHC class I and class II  
XX antigen expression. The TSU sequence contains motifs related to IFN  
XX signalling (GAS, ISRE and interleukin-4 response elements). The nucleic  
XX acid can be used to regulate gene expression in a subject, e.g. a human  
XX or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7  
XX -1, B7-2, FC gamma R, IL-2 or HIV gene expression. It can be used to  
XX inhibit transplant rejection, or treat an autoimmune or inflammatory  
XX disease or disorder. It can also be used to inhibit the action of STAT1-  
XX 6, or a cytokine

XX SQ Sequence 14 BP; 1 A; 1 C; 1 G; 5 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

DB 11 YYY 13

```

RESULT 176
AAV22311/c
ID AAV22311 standard; cDNA; 14 BP.
XX
XX AAV22311;
AC
XX
XX 29-JUN-1998 (first entry)
DT
XX
XX ISRE gene promoter motif found in a trophoblast STAT utron.
DE
XX
XX Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW antigen expression; gene promoter; class I; class II; IFN signalling;
KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW autoimmune disease; inflammatory disease; ss.
XX
XX Unidentified.
OS
XX WO9744450-A1.
PN
XX
XX 27-NOV-1997.
PD
XX
XX 21-MAY-1997; 97WO-US009459.
PF
XX
XX 21-MAY-1996; 96US-00646789.
PR
XX
XX (UYA ) UNIV YALE.
PA
XX
XX Peyman JA;
PI
XX
XX WPI; 1998-018505/02.
DR
XX
XX Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT suppress express expression from promoter of interest, specifically TSU
PT nucleic acid suppression of MHC Class I and II gene expression.
XX
XX Disclosure; Page 89; 200pp; English.
PS
XX
XX The present sequence represents an ISRE gene promoter motif found in a
CC trophoblast STAT utron (TSU). TSUs be isolated from a CDNA library
CC prepared from mRNA isolated from trophoblast cells. Utrons are from, or
CC are homologous to, the 3' untranslated region (UTR), of an mRNA that
CC stimulates or inhibits a cellular response by sequence specific
CC interactions. The TSU is able to suppress constitutive and interferon-
CC gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC and class II antigen expression and expression of other antigens, the
CC gene promoters of which contain related sequence motifs that are
CC stimulated by the same factors which stimulate MHC class I and class II
CC antigen expression. The TSU sequence contains motifs related to IFN
CC signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC acid can be used to regulate gene expression in a subject, e.g. a human
CC or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC inhibit transplant rejection, or treat an autoimmune or inflammatory
CC disease or disorder. It can also be used to inhibit the action of STAT1-
CC 6, or a cytokine
XX
XX Sequence 14 BP; 1 A; 1 C; 1 G; 5 T; 0 U; 6 Other;
SQ
Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 14 RRR 12
RESULT 177
AAV22312
ID AAV22312 standard; RNA; 14 BP.
XX
XX
XX 29-JUN-1998 (first entry)
DT
XX
XX ISRE complement sequence found in the TSUs of the invention.
DE
XX
XX Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW antigen expression; gene promoter; class I; class II; IFN signalling;
KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW autoimmune disease; inflammatory disease; ss.
XX
XX Unidentified.
OS
XX WO9744450-A1.
PN
XX
XX 27-NOV-1997.
PD
XX
XX 21-MAY-1997; 97WO-US009459.
PF
XX
XX 21-MAY-1996; 96US-00646789.
PR
XX
XX (UYA ) UNIV YALE.
PA
XX
XX Peyman JA;
PI
XX
XX WPI; 1998-018505/02.
DR
XX
XX Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT suppress express expression from promoter of interest, specifically TSU
PT nucleic acid suppression of MHC Class I and II gene expression.
XX
XX Disclosure; Page 89; 200pp; English.
PS
XX
XX The present sequence represents an ISRE complement sequence found in the
CC trophoblast STAT utrons (TSUs) of the invention. Utrons are from, or are
CC homologous to, the 3' untranslated region (UTR), of an mRNA that
CC stimulates or inhibits a cellular response by sequence specific
CC interactions. The TSU is able to suppress constitutive and interferon-
CC gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC and class II antigen expression and expression of other antigens, the
CC gene promoters of which contain related sequence motifs that are
CC stimulated by the same factors which stimulate MHC class I and class II
CC antigen expression. The TSU sequence contains motifs related to IFN
CC signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC acid can be used to regulate gene expression in a subject, e.g. a human
CC or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC inhibit transplant rejection, or treat an autoimmune or inflammatory
CC disease or disorder. It can also be used to inhibit the action of STAT1-
CC 6, or a cytokine
XX
XX Sequence 14 BP; 5 A; 1 C; 1 G; 1 T; 0 U; 6 Other;
SQ
Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 1 RRR 3
RESULT 178
AAV22312/c
ID AAV22312 standard; RNA; 14 BP.
XX
XX
XX AAV22312;
AC
XX
XX 29-JUN-1998 (first entry)
DT
XX
XX ISRE complement sequence found in the TSUs of the invention.
DE

```

XX Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;  
 KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
 KW antigen expression; gene promoter; class I; class II; IFN signalling;  
 KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;  
 KW B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;  
 KW autoimmune disease; inflammatory disease; ss.  
 XX Unidentified.  
 OS  
 XX  
 XX W09744450-A1.  
 PN  
 XX  
 XX 27-NOV-1997.  
 PD  
 XX  
 XX 21-MAY-1997; 97WO-US009459.  
 PF  
 XX  
 XX 21-MAY-1996; 96US-00646789.  
 PR  
 XX  
 XX (UYA ) UNIV YALE.  
 PA  
 XX  
 XX Peyman JA;  
 PI  
 XX  
 XX WPI; 1998-018505/02.  
 DR  
 XX  
 XX Utrons, RNA molecules containing promoter regulatory motifs - useful to  
 PT suppress express expression from promoter of interest. specifically TSU  
 PT nucleic acid suppression of MHC Class I and II gene expression.  
 PT  
 XX  
 XX Disclosure; Page 89; 200pp; English.  
 PS  
 XX  
 XX The present sequence represents an ISRE complement sequence found in the  
 CC trophoblast STAT utrons (TSUs) of the invention. Utrons are from, or are  
 CC homologous to, the 3' untranslated region (UTR), of an mRNA that  
 CC stimulates or inhibits a cellular response by sequence specific  
 CC interactions. The TSU is able to suppress constitutive and interferon-  
 CC gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I  
 CC and class II antigen expression and expression of other antigens, the  
 CC gene promoters of which contain related sequence motifs that are  
 CC stimulated by the same factors which stimulate MHC class I and class II  
 CC antigen expression. The TSU sequence contains motifs related to IFN  
 CC signalling (GAS, ISRE and interleukin-4 response elements). The nucleic  
 CC acid can be used to regulate gene expression in a subject, e.g. a human  
 CC or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7  
 CC -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to  
 CC inhibit transplant rejection, or treat an autoimmune or inflammatory  
 CC disease or disorder. It can also be used to inhibit the action of STAT1-  
 CC 6, or a cytokine  
 XX  
 XX Sequence 14 BP; 5 A; 1 C; 1 G; 1 T; 0 U; 6 Other;  
 SQ  
 Query Match 30.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 Db ||||  
 4 YYY 2  
 RESULT 179  
 AA243723  
 ID AA243723 standard; DNA; 14 BP.  
 XX  
 XX AA243723;  
 AC  
 XX  
 XX 24-FEB-2000 (first entry)  
 DT  
 XX  
 XX Human FSH-beta splice-acceptor site DNA motif.  
 DE  
 XX FSH-beta; human; follicle stimulating hormone-beta; gene therapy;  
 KW delivery system; treatment; infertility; fertility enhancer; ss.  
 XX  
 XX Homo sapiens.  
 OS

XX WO9957263-A1.  
 PN  
 XX 11-NOV-1999.  
 PD  
 XX  
 XX 05-MAY-1999; 99WO-US009795.  
 PF  
 XX  
 XX 07-MAY-1998; 98US-0084663P.  
 PR  
 XX  
 XX (TRAN-) TRANSGARYOTIC THERAPIES INC.  
 PA  
 XX Treco DA, Heartlein MW, Selden RF;  
 PI  
 XX WPI; 2000-052968/04.  
 DR  
 XX  
 XX Novel DNA construct used to produce recombinant cells useful for in vitro  
 PT protein production and gene therapy.  
 PT  
 XX  
 XX Disclosure; Page 64; 70pp; English.  
 PS  
 XX  
 XX This invention describes a novel DNA construct (A) that alters expression  
 CC of an endogenous follicle stimulating hormone (FSH)-beta gene in a  
 CC mammalian cell upon integration into the genome of the cell via  
 CC homologous recombination. Homologously recombinant cells of the invention  
 CC which express follicle-stimulating hormone beta (FSHbeta) are useful for  
 CC in vitro production of the protein and gene therapy. The cells are also  
 CC useful as populations of homologously recombinant cell lines, as  
 CC populations of homologously recombinant primary or secondary cells, as  
 CC homologously recombinant clonal cells or strains, as homologously  
 CC recombinant heterogeneous cell strains or lines, and as cell mixtures of  
 CC any of the above. Such cells may be used in a delivery system for  
 CC treating infertility, for enhancing fertility in a human or animal, or  
 CC for treating any other conditions treatable with FSHbeta. The  
 CC polynucleotides may be used as a source of primers, and to alter the  
 CC expression of an endogenous FSHbeta gene. This sequence represents a  
 CC human FSH-beta gene splice-acceptor site DNA motif which is used in the  
 CC method of the invention  
 XX  
 XX Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;  
 SQ  
 Query Match 30.0%; Score 3; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 Db ||||  
 1 YYY 3  
 RESULT 180  
 AA243723/C  
 ID AA243723 standard; DNA; 14 BP.  
 XX  
 XX AA243723;  
 AC  
 XX  
 XX 24-FEB-2000 (first entry)  
 DT  
 XX  
 XX Human FSH-beta splice-acceptor site DNA motif.  
 DE  
 XX FSH-beta; human; follicle stimulating hormone-beta; gene therapy;  
 KW delivery system; treatment; infertility; fertility enhancer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9957263-A1.  
 PN  
 XX 11-NOV-1999.  
 PD  
 XX  
 XX 05-MAY-1999; 99WO-US009795.  
 PF  
 XX  
 XX 07-MAY-1998; 98US-0084663P.  
 PR  
 XX  
 XX (TRAN-) TRANSGARYOTIC THERAPIES INC.  
 PA



XX Treco DA, Heartlein MW, Selden RF;  
 XX WPI; 2000-052968/04.  
 XX Novel DNA construct used to produce recombinant cells useful for in vitro  
 XX protein production and gene therapy.  
 XX Disclosure; Page 64; 70pp; English.  
 XX This invention describes a novel DNA construct (A) that alters expression  
 XX of an endogenous follicle stimulating hormone (FSH)-beta gene in a  
 XX mammalian cell upon integration into the genome of the cell via  
 XX homologous recombination. Homologously recombinant cells of the invention  
 XX which express follicle-stimulating hormone beta (FSHbeta) are useful for  
 XX in vitro production of the protein and gene therapy. The cells are also  
 XX useful as populations of homologously recombinant cell lines, as  
 XX populations of homologously recombinant primary or secondary cells, as  
 XX homologously recombinant clonal cells or strains, as homologously  
 XX recombinant heterogeneous cell strains or lines, and as cell mixtures of  
 XX any of the above. Such cells may be used in a delivery system for  
 XX treating infertility, for enhancing fertility in a human or animal, or  
 XX for treating any other conditions treatable with FSHbeta. The  
 XX polynucleotides may be used as a source of primers, and to alter the  
 XX expression of an endogenous FSHbeta gene. This sequence represents a  
 XX human FSH-beta gene splice-acceptor site DNA motif which is used in the  
 XX method of the invention  
 XX  
 XX Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;  
 XX  
 XX Query Match 30.0%; Score 3; DB 3; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 RRR 3  
 XX ||||  
 XX 10 RRR 8  
 XX  
 XX RESULT 181  
 XX AAA91879  
 XX ID AAA91879 standard; DNA; 14 BP.  
 XX AC AAA91879;  
 XX DT 08-JAN-2001 (first entry)  
 XX DE Complement of SNP site beginning at position 211 of the TGF-b1 gene.  
 XX KW TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;  
 XX KW single nucleotide polymorphism; SNP; human; primer; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT variation replace(6,G)  
 XX FT /\*tag= a  
 XX FT /standard\_name= "Single nucleotide polymorphism"  
 XX FT  
 XX FT WO200049169-A1.  
 XX PN 24-AUG-2000.  
 XX PD 18-FEB-2000; 2000WO-US004251.  
 XX PF 19-FEB-1999; 99US-0120787P.  
 XX PR (DZGE-) DZGENES LLC.  
 XX PA Moskowitz DW;  
 XX PI WPI; 2000-549279/50.  
 XX DR  
 XX  
 XX Diagnosing genetic susceptibility for end-stage renal disease using  
 XX single nucleotide polymorphisms, involves analyzing sample obtained from  
 XX subject to detect genetic polymorphism in the sample polynucleotide.  
 XX Example 3; Page 37; 73pp; English.  
 XX The present invention relates the diagnosis of genetic susceptibility for  
 XX end-stage renal disease (ESRD). The method involves analysing a  
 XX polynucleotide sample for a single nucleotide polymorphism (SNP)  
 XX associated with an altered susceptibility for ESRD. The method allows  
 XX early detection of ESRD and hence effective delay or ideally, prevention  
 XX of ESRD is made possible. The present sequence is a SNP site found in the  
 XX human TGF-b1 promoter sequence (see AAA91866). Polymorphisms in this gene  
 XX are known to be a probable trigger for renal apoptosis  
 XX  
 XX Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;  
 XX  
 XX Query Match 30.0%; Score 3; DB 3; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 8 YYY 10  
 XX ||||  
 XX 6 YYY 8  
 XX  
 XX RESULT 182  
 XX AAA91879/C  
 XX ID AAA91879 standard; DNA; 14 BP.  
 XX AC AAA91879;  
 XX DT 08-JAN-2001 (first entry)  
 XX DE Complement of SNP site beginning at position 211 of the TGF-b1 gene.  
 XX KW TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;  
 XX KW single nucleotide polymorphism; SNP; human; primer; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT variation replace(6,G)  
 XX FT /\*tag= a  
 XX FT /standard\_name= "Single nucleotide polymorphism"  
 XX FT  
 XX FT WO200049169-A1.  
 XX PN 24-AUG-2000.  
 XX PD 18-FEB-2000; 2000WO-US004251.  
 XX PF 19-FEB-1999; 99US-0120787P.  
 XX PR (DZGE-) DZGENES LLC.  
 XX PA Moskowitz DW;  
 XX PI WPI; 2000-549279/50.  
 XX DR  
 XX  
 XX Diagnosing genetic susceptibility for end-stage renal disease using  
 XX single nucleotide polymorphisms, involves analyzing sample obtained from  
 XX subject to detect genetic polymorphism in the sample polynucleotide.  
 XX Example 3; Page 37; 73pp; English.  
 XX The present invention relates the diagnosis of genetic susceptibility for  
 XX end-stage renal disease (ESRD). The method involves analysing a  
 XX polynucleotide sample for a single nucleotide polymorphism (SNP)  
 XX associated with an altered susceptibility for ESRD. The method allows  
 XX early detection of ESRD and hence effective delay or ideally, prevention  
 XX of ESRD is made possible. The present sequence is a SNP site found in the  
 XX human TGF-b1 promoter sequence (see AAA91866). Polymorphisms in this gene  
 XX are known to be a probable trigger for renal apoptosis

CC are known to be a probable trigger for renal apoptosis  
 XX  
 SQ Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
 |||  
 Db 8 RRR 6

## RESULT 183

AAAD17448  
 ID AAD17448 standard; DNA; 14 BP.

AC AAD17448;

DT 10-DEC-2001 (first entry)

XX Splice acceptor site which directs the splicing of one exon to another.  
 XX Mutation; homologous recombination; target sequence; gene therapy;  
 KW homologous recombination-enhancing agent; non-homologous end joining;  
 KW therapeutic protein; splice acceptor site; ds.

XX Unidentified.

XX WO200168882-A2.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US007870.

XX 14-MAR-2000; 2000US-00525160.

XX (TRAN-) TRANSKARYOTIC THERAPIES INC.

XX Ivanov E;

XX WPI; 2001-582459/65.

XX Complex or composition comprising a double stranded DNA sequence, a  
 PT homologous recombination-enhancing agent, and agent inhibiting non-  
 PT homologous end joining, for promoting alteration of a target sequence in  
 PT a cell.

XX Disclosure; Page 50; 82pp; English.

XX The invention relates to a complex for promoting alteration of a target  
 CC sequence in a cell, comprising a double stranded DNA sequence, a  
 CC homologous recombination-enhancing agent and an agent inhibiting non-  
 CC homologous end joining. The invention is used in gene therapy. The  
 CC complex is useful for promoting an alteration at a selected site of a  
 CC target sequence of a cell preferably of fungal, plant or animal origin,  
 CC or of vertebrate origin which is a primary or secondary mammalian (human)  
 CC cell or an immortalised mammalian (human) cell, where target sequence  
 CC comprises a mutation preferably point mutation having less than 10 base  
 CC pairs which differ from wild-type sequence, (selected from cystic  
 CC fibrosis transmembrane regulator (CFTR) gene having mutation changes in  
 CC an amino acid encoded by codon 508, beta-globin gene having mutation  
 CC changes in an amino acid encoded by codon 6, Factor VIII gene having  
 CC mutation changes in an amino acid encoded by codon 2209 or 2229, Factor  
 CC IX gene, von Willebrand factor gene or xeroderma pigmentosa group G gene)  
 CC ; and the DNA sequence comprises a wild-type sequence which can correct  
 CC the mutation. The method further comprises introducing an agent which  
 CC inhibits a mismatch-repair protein (expression) which is from Msh2,  
 CC Msh6, Msh3, Mlh1 and PMS2. Or is an anti-mismatch-repair protein antibody  
 CC covalently linked to the DNA sequence, or to Rad52 protein or its  
 CC fragment. The complex is useful for altering expression of a protein  
 CC coding sequence of a gene in a cell. The method comprises introducing the  
 CC complex into the cell, where the DNA sequence comprises a regulatory

CC sequence, maintaining the cell under conditions which permit alteration  
 CC of a targetted genomic sequence to produce a homologously recombinant  
 CC cell and maintaining the homologously recombinant cell under conditions  
 CC which permit expression of the protein coding sequence of the gene under  
 CC control of the regulatory sequence. Homologously recombinant cell is  
 CC useful as a vehicle or delivery system for therapeutic proteins, such as  
 CC enzymes, hormones, cytokines, antigens, antibodies, clotting factors,  
 CC anti-sense RNA, regulatory proteins, transcription proteins, receptors,  
 CC structural proteins, novel (non-optimised) proteins and nucleic acid  
 CC products and engineered DNA and for supplying a therapeutic protein,  
 CC including erythropoietin, calcitonin, growth hormone, insulin and  
 CC insulinotropin. The present sequence is a splice acceptor site, used in  
 CC the invention. This sequence directs the splicing of one exon to another  
 CC exon

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

Query Match 30.0%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
 |||  
 Db 1 YYY 3

## RESULT 184

AAAD17448/c

ID AAD17448 standard; DNA; 14 BP.

XX AAD17448;

XX 10-DEC-2001 (first entry)

XX Splice acceptor site which directs the splicing of one exon to another.  
 XX Mutation; homologous recombination; target sequence; gene therapy;  
 KW homologous recombination-enhancing agent; non-homologous end joining;  
 KW therapeutic protein; splice acceptor site; ds.

XX Unidentified.

XX WO200168882-A2.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US007870.

XX 14-MAR-2000; 2000US-00525160.

XX (TRAN-) TRANSKARYOTIC THERAPIES INC.

XX Ivanov E;

XX WPI; 2001-582459/65.

XX Complex or composition comprising a double stranded DNA sequence, a  
 PT homologous recombination-enhancing agent, and agent inhibiting non-  
 PT homologous end joining, for promoting alteration of a target sequence in  
 PT a cell.

XX Disclosure; Page 50; 82pp; English.

XX The invention relates to a complex for promoting alteration of a target  
 CC sequence in a cell, comprising a double stranded DNA sequence, a  
 CC homologous recombination-enhancing agent and an agent inhibiting non-  
 CC homologous end joining. The invention is used in gene therapy. The  
 CC complex is useful for promoting an alteration at a selected site of a  
 CC target sequence of a cell preferably of fungal, plant or animal origin,  
 CC or of vertebrate origin which is a primary or secondary mammalian (human)  
 CC cell or an immortalised mammalian (human) cell, where target sequence  
 CC comprises a mutation preferably point mutation having less than 10 base  
 CC pairs which differ from wild-type sequence, (selected from cystic

CC fibrosis transmembrane regulator (CFTR) gene having mutation changes in  
CC an amino acid encoded by codon 508, beta-globin gene having mutation  
CC changes in an amino acid encoded by codon 6, Factor VIII gene having  
CC mutation changes in an amino acid encoded by codon 2209 or 2229, Factor  
CC IX gene, von Willebrand factor gene or xeroderma pigmentosa group G gene)  
CC ; and the DNA sequence comprises a wild-type sequence which can correct  
CC the mutation. The method further comprises introducing an agent which  
CC inhibits a mismatch-repair protein (expression), which is from Msh2,  
CC Msh6, Msh3, Mlh1 and PMS2. Or is an anti-mismatch-repair protein antibody  
CC covalently linked to the DNA sequence, or to Rad52 protein or its  
CC fragment. The complex is useful for altering expression of a protein  
CC coding sequence of a gene in a cell. The method comprises introducing the  
CC complex into the cell, where the DNA sequence comprises a regulatory  
CC sequence, maintaining the cell under conditions which permit alteration  
CC of a targeted genomic sequence to produce a homologously recombinant  
CC cell and maintaining the homologously recombinant cell under conditions  
CC which permit expression of the protein coding sequence of the gene under  
CC control of the regulatory sequence. Homologously recombinant cell is  
CC useful as a vehicle or delivery system for therapeutic proteins, such as  
CC enzymes, hormones, cytokines, antigens, antibodies, clotting factors,  
CC anti-sense RNA, regulatory proteins, transcription proteins, receptors,  
CC structural proteins, novel (non-optimised) proteins and nucleic acid  
CC products and engineered DNA and for supplying a therapeutic protein,  
CC including erythropoietin, calcitonin, growth hormone, insulin and  
CC insulinotropin. The present sequence is a splice acceptor site, used in  
CC the invention. This sequence directs the splicing of one exon to another  
CC exon

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

Query Match 30.0%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

## RESULT 185

ABA99069  
ID ABA99069 standard; DNA; 14 BP.

AC ABA99069;

DT 03-JUL-2002 (first entry)

XX Gut-enriched Krueppel-like factor binding site (complementary strand).

DE TGF-beta 1; transforming growth factor-beta 1; cytostatic; hypotensive;  
KW cardiant; vasotropic; antiarteriosclerotic; antidiabetic; nephrotropic;  
KW antialcoholic; tranquilliser; antiasthmatic; gene therapy; cancer;  
KW hypertension; GKLF; gut-enriched Krueppel-like factor; ds.

XX Synthetic.

XX Key Location/Qualifiers  
FH variation replace(6,G)  
FT /\*tag= a

FT /standard name= "Single nucleotide polymorphism"  
FT /note= "This is a SNP in the human TGFbeta1 promoter"

XX WO200208468-A1.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-US023368.

XX 25-JUL-2000; 2000US-0220583P.

XX (DZGE-) DZ GENES LLC.

XX Moskowitz DW;

XX WPI; 2002-241578/29.  
DR Novel nucleic acid molecule comprising a single nucleotide polymorphism  
XX at a specified position in transforming growth factor-beta 1 promoter  
PT region, useful for diagnosing cancers, hypertension and other diseases.  
XX Example 2; Page 38; 6'pp; English.

XX The sequence represents the complement of the human transforming growth  
CC factor-beta 1 promoter region gut-enriched Krueppel-like factor (GKLF)  
CC site. The invention relates to a novel isolated polynucleotide containing  
CC at least one single nucleotide polymorphism (SNP) at position 216 or 563  
CC of TGF-beta1, where the SNP is associated with a disease, condition or  
CC disorder. The polynucleotide has cytostatic, hypotensive, cardiant,  
CC vasotropic, antiarteriosclerotic, antidiabetic, nephrotropic,  
CC antialcoholic, tranquilliser, and antiasthmatic activity. The  
CC polynucleotide may have a use in gene therapy. The method provided in the  
CC invention is useful for diagnosing genetic susceptibility for cancers,  
CC hypertension and a variety of other diseases. The polynucleotide is  
CC useful for designing prophylactic treatment regimes for patients  
CC determined to have an increased susceptibility to these diseases

XX SQ Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 6 YYY 8

## RESULT 186

ABA99069/C  
ID ABA99069 standard; DNA; 14 BP.

AC ABA99069;

DT 03-JUL-2002 (first entry)

XX Gut-enriched Krueppel-like factor binding site (complementary strand).

DE TGF-beta 1; transforming growth factor-beta 1; cytostatic; hypotensive;  
KW cardiant; vasotropic; antiarteriosclerotic; antidiabetic; nephrotropic;  
KW antialcoholic; tranquilliser; antiasthmatic; gene therapy; cancer;  
KW hypertension; GKLF; gut-enriched Krueppel-like factor; ds.

XX Synthetic.

XX Key Location/Qualifiers  
FH variation replace(6,G)  
FT /\*tag= a

FT /standard name= "Single nucleotide polymorphism"  
FT /note= "This is a SNP in the human TGFbeta1 promoter"

XX WO200208468-A1.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-US023368.

XX 25-JUL-2000; 2000US-0220583P.

XX (DZGE-) DZ GENES LLC.

XX Moskowitz DW;

XX WPI; 2002-241578/29.

XX Novel nucleic acid molecule comprising a single nucleotide polymorphism  
PT at a specified position in transforming growth factor-beta 1 promoter

region, useful for diagnosing cancers, hypertension and other diseases.  
 Example 2; Page 38; 67pp; English.

The sequence represents the complement of the human transforming growth factor-beta 1 promoter region gut-enriched Krueppel-like factor (GKLF) site. The invention relates to a novel isolated polynucleotide containing at least one single nucleotide polymorphism (SNP) at position 216 or 563 of TGF-beta1, where the SNP is associated with a disease, condition or disorder. The polynucleotide has cystostatic, hypotensive, cardiant, vasotropic, antiarteriosclerotic, and antidiabetic, nephrotropic, antialcoholic, tranquilizer, and antiasthmatic activity. The polynucleotide may have a use in gene therapy. The method provided in the invention is useful for diagnosing genetic susceptibility for cancers, hypertension and a variety of other diseases. The polynucleotide is useful for designing prophylactic treatment regimes for patients determined to have an increased susceptibility to these diseases

Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;  
 Query Match 30.0%; Score 3; DB 6; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
 ||||  
 Db 8 RRR 6

## RESULT 187

ADP83663  
 ID ADF83663 standard; DNA; 14 BP.

AC ADF83663;

DT 26-FEB-2004 (first entry)

DE Pravastatin production related primer, P450R2.

KW mevastatin; pravastatin; lactone ring-closed body; ss; primer.

OS Unidentified.

PN JP2002247984-A.

PD 03-SEP-2002.

PF 23-FEB-2001; 2001JP-00047664.

PR 23-FEB-2001; 2001JP-00047664.

PA (SAOC ) MERCIAN CORP.

XX WPI; 2004-084761/09.

XX A DNA participating in the production of pravastatin, a recombinant plasmid, a transformant, production of pravastatin.

PS Example 1; SEQ ID NO 4; 15pp; Japanese.

XX The invention relates to novel isolated pure DNA containing a gene participating in the biological conversion of mevastatin to pravastatin, its salt or its lactone ring-closed body or a mutant having a function of hybridizing with the gene under a stringent condition and giving the conversion activity to Streptomyces lividans. The invention further relates to an isolated pure DNA containing a gene participating in the biological conversion of mevastatin, its lactone ring-open body or its salt which can be prepared from a microbe of Microtetraspora genus to pravastatin, its salt or its lactone ring-closed body or a mutant having a function of hybridizing with the gene under a stringent condition and giving the conversion activity to Streptomyces lividans. The method is used for the preparation of pravastatin, its salt or its lactone ring-closed body. This polynucleotide sequence represents a primer relating to

CC the production of pravastatin of the invention.  
 XX  
 SQ Sequence 14 BP; 2 A; 3 C; 1 G; 3 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
 ||||  
 Db 11 RRC 13

## RESULT 188

ADP83663/C  
 ID ADF83663 standard; DNA; 14 BP.

AC ADF83663;

XX 26-FEB-2004 (first entry)

DE Pravastatin production related primer, P450R2.

KW mevastatin; pravastatin; lactone ring-closed body; ss; primer.

OS Unidentified.

PN JP2002247984-A.

PD 03-SEP-2002.

PF 23-FEB-2001; 2001JP-00047664.

PR 23-FEB-2001; 2001JP-00047664.

PA (SAOC ) MERCIAN CORP.

XX WPI; 2004-084761/09.

XX A DNA participating in the production of pravastatin, a recombinant plasmid, a transformant, production of pravastatin.

PS Example 1; SEQ ID NO 4; 15pp; Japanese.

XX The invention relates to novel isolated pure DNA containing a gene participating in the biological conversion of mevastatin to pravastatin, its salt or its lactone ring-closed body or a mutant having a function of hybridizing with the gene under a stringent condition and giving the conversion activity to Streptomyces lividans. The invention further relates to an isolated pure DNA containing a gene participating in the biological conversion of mevastatin, its lactone ring-open body or its salt which can be prepared from a microbe of Microtetraspora genus to pravastatin, its salt or its lactone ring-closed body or a mutant having a function of hybridizing with the gene under a stringent condition and giving the conversion activity to Streptomyces lividans. The method is used for the preparation of pravastatin, its salt or its lactone ring-closed body. This polynucleotide sequence represents a primer relating to

XX Sequence 14 BP; 2 A; 3 C; 1 G; 3 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
 ||||  
 Db 13 GY 11

## RESULT 189

AAT96081  
 ID AAT96081 standard; DNA; 15 BP.

```

XX AC AAT96081;
XX DT 31-MAR-1998 (first entry)
XX DE Recombination region homologous to SINE flanking region.
XX KW Recombination region; consensus defined flanking region;
XX KW short interspersed repeated DNA element; SINE; ss.
XX OS Synthetic.
XX PN US5695977-A.
XX PN 09-DEC-1997.
XX PD 07-MAY-1996; 96US-00643886.
XX PF 31-AUG-1995; 95US-0003063P.
XX PR (GENE-) GENETIC INFORMATION RES INST.
XX PA Jurka JW;
XX PI WPI; 1998-041303/04.
XX DR WPI; 1998-041303/04.
XX DT Genomic integration of DNA by site directed recombination - using
XX DE construct containing recombination region homologous to consensus defined
XX KW flanking region of short interspersed repeated DNA element.
XX KW Claim 7; Col 17-18; 12pp; English.
XX CC Integrating a DNA sequence into the genome of a vertebrate host cell,
XX CC comprises introducing a construct comprising the DNA sequence and a
XX CC recombination region homologous to a consensus defined flanking region of
XX CC a short interspersed repeated DNA element (SINE), e.g. the present
XX CC sequence. The method may be used to modify the phenotype of cells, or
XX CC investigate the response of receptors, metabolic pathways or expression
XX CC products involved in the regulation of transcription or transduction of
XX CC signals. It may also be used to produce protein products and transgenic
XX CC animals, by providing novel capabilities to the cells or inhibiting
XX CC endogenous capabilities, investigate physiological indications and screen
XX CC cosmetics, foods and drugs. By using antisense sequences effective
XX CC inhibition of both copies of a gene is possible, ensuring the substantial
XX CC absence of the particular transcriptional or translational product. In
XX CC addition the method may enhance efficiency in gene therapy, when
XX CC providing for a capability in which the host is deficient
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 11 Other;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRR 3
Db 12 RRR 14

RESULT 190
AAT96081/c
ID AAT96081 standard; DNA; 15 BP.
XX AC AAT96081;
XX DT 31-MAR-1998 (first entry)
XX DE Recombination region homologous to SINE flanking region.
XX KW Recombination region; consensus defined flanking region;
XX KW short interspersed repeated DNA element; SINE; ss.
XX OS Synthetic.

```

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XX PN US5695977-A.
XX DT 09-DEC-1997.
XX DE 07-MAY-1996; 96US-00643886.
XX PF 31-AUG-1995; 95US-0003063P.
XX PR (GENE-) GENETIC INFORMATION RES INST.
XX PA Jurka JW;
XX PI WPI; 1998-041303/04.
XX DR WPI; 1998-041303/04.
XX DT Genomic integration of DNA by site directed recombination - using
XX DE construct containing recombination region homologous to consensus defined
XX KW flanking region of short interspersed repeated DNA element.
XX KW Claim 7; Col 17-18; 12pp; English.
XX CC Integrating a DNA sequence into the genome of a vertebrate host cell,
XX CC comprises introducing a construct comprising the DNA sequence and a
XX CC recombination region homologous to a consensus defined flanking region of
XX CC a short interspersed repeated DNA element (SINE), e.g. the present
XX CC sequence. The method may be used to modify the phenotype of cells, or
XX CC investigate the response of receptors, metabolic pathways or expression
XX CC products involved in the regulation of transcription or transduction of
XX CC signals. It may also be used to produce protein products and transgenic
XX CC animals, by providing novel capabilities to the cells or inhibiting
XX CC endogenous capabilities, investigate physiological indications and screen
XX CC cosmetics, foods and drugs. By using antisense sequences effective
XX CC inhibition of both copies of a gene is possible, ensuring the substantial
XX CC absence of the particular transcriptional or translational product. In
XX CC addition the method may enhance efficiency in gene therapy, when
XX CC providing for a capability in which the host is deficient
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 11 Other;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 YYY 10
Db 14 YYY 12

RESULT 191
AAT96069
ID AAT96069 standard; DNA; 15 BP.
XX AC AAT96069;
XX DT 31-MAR-1998 (first entry)
XX DE Recombination region homologous to SINE flanking region.
XX KW Recombination region; consensus defined flanking region;
XX KW short interspersed repeated DNA element; SINE; ss.
XX OS Synthetic.
XX PN US5695977-A.
XX PN 09-DEC-1997.
XX PF 07-MAY-1996; 96US-00643886.
XX PR 31-AUG-1995; 95US-0003063P.
XX PR (GENE-) GENETIC INFORMATION RES INST.
XX OS

```

PI Jurka JW;  
 XX WPI; 1998-041303/04.  
 XX  
 XX Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 XX Claim 1; Col 13-14; 12pp; English.  
 XX  
 XX Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient  
 XX  
 XX Sequence 15 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 9 Other;  
 SQ

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 YYY 10  
 DB 12 YYY 14

RESULT 192  
 AAT96069/c  
 ID AAT96069 standard; DNA; 15 BP.  
 XX  
 AC AAT96069;  
 DT 31-MAR-1998 (first entry)  
 XX  
 DE Recombination region homologous to SINE flanking region.  
 XX  
 XX Recombination region; consensus defined flanking region;  
 KW short interspersed repeated DNA element; SINE; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5695977-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 XX 07-MAY-1996; 96US-00643886.  
 XX  
 PR 31-AUG-1995; 95US-0003063P.  
 XX  
 XX (GENE-) GENETIC INFORMATION RES INST.  
 PA  
 XX Jurka JW;  
 XX  
 XX WPI; 1998-041303/04.  
 XX  
 XX Genomic integration of DNA by site directed recombination - using  
 PT construct containing recombination region homologous to consensus defined  
 PT flanking region of short interspersed repeated DNA element.  
 XX  
 XX Claim 1; Col 13-14; 12pp; English.  
 XX  
 XX Integrating a DNA sequence into the genome of a vertebrate host cell,  
 CC comprises introducing a construct comprising the DNA sequence and a  
 CC recombination region homologous to a consensus defined flanking region of  
 CC a short interspersed repeated DNA element (SINE), e.g. the present  
 CC sequence. The method may be used to modify the phenotype of cells, or  
 CC investigate the response of receptors, metabolic pathways or expression  
 CC products involved in the regulation of transcription or transduction of  
 CC signals. It may also be used to produce protein products and transgenic  
 CC animals, by providing novel capabilities to the cells or inhibiting  
 CC endogenous capabilities, investigate physiological indications and screen  
 CC cosmetics, foods and drugs. By using antisense sequences effective  
 CC inhibition of both copies of a gene is possible, ensuring the substantial  
 CC absence of the particular transcriptional or translational product. In  
 CC addition the method may enhance efficiency in gene therapy, when  
 CC providing for a capability in which the host is deficient  
 XX  
 XX Sequence 15 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 9 Other;  
 SQ

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRR 3  
 DB 14 RRR 12

RESULT 193  
 AAF75852  
 ID AAF75852 standard; DNA; 15 BP.  
 XX  
 AC AAF75852;  
 DT 18-MAY-2001 (first entry)  
 XX  
 DE 3' splice junction consensus sequence used to design PCR primers.  
 XX  
 KW 3' splice junction consensus sequence; PCR primer design; ds.  
 OS Unidentified.  
 XX  
 PN WO200116350-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 XX 01-SEP-2000; 2000WO-US024122.  
 PF  
 XX 01-SEP-1999; 99US-0151975P.  
 PR  
 XX 01-NOV-1999; 99US-00431451.  
 XX  
 XX (GENO-) GENOME TECHNOLOGIES LLC.  
 PA  
 XX Senapathy P;  
 PI  
 XX WPI; 2001-226695/23.  
 DR  
 XX  
 XX Amplifying desired regions of nucleic acid, especially exons from a  
 PT genomic DNA sample, comprises using a partly-fixed consensus first primer  
 PT and partly-fixed second primer, both having a sequence of randomized  
 PT nucleotides.  
 XX  
 XX Disclosure; Fig 2; 52pp; English.  
 PS  
 XX The present invention relates to a method for amplifying a region of  
 CC nucleic acid from a sample via PCR using several primers. The primers of  
 CC the present invention have a region of fixed nucleotide sequence  
 CC identical or complementary to a consensus sequence of interest and also  
 CC have a region of randomized nucleotide sequence. The present sequence is  
 CC the 3' splice junction consensus sequence, which was used to design PCR  
 CC primers for use in the present invention. The method is useful for  
 CC specifically amplifying a desired region of a nucleic acid, especially  
 CC exons from a sample of DNA. The method is also applicable for amplifying  
 CC regions flanking a consensus sequence in a sample of nucleic acid of  
 CC totally or partially unknown sequence

```
XX SQ Sequence 15 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 9 Other;
Query Match 30.0%; Score 3; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 5 YYY 7
|||

RESULT 194
AAF75852/c
ID AAF75852 standard; DNA; 15 BP.
XX AC
XX DT 12-PEB-2004 (revised)
XX DT 18-SEP-2003 (first entry)
XX DE Beta-globin stabilising RNA motif.
XX KW tumour antigen; cancer; beta-globin; cytokine; RNase inhibitor; RNasin;
XX KW vaccine; cytostatic; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT misc_feature 5
XX FT /*tag= a
XX FT /note= "Can be repeated n times where n is an undisclosed
XX FT figure"
XX FT 10
XX FT misc_feature b
XX FT /*tag= b
XX FT /note= "Can be repeated n times where n is an undisclosed
XX FT figure"
XX PN WO2003051401-A2.
XX PD 26-JUN-2003.
XX PF 19-DEC-2002; 2002WO-EP014577.
XX PR 19-DEC-2001; 2001DE-01062480.
XX PA (CURE-) CUREVAC GMBH.
XX PI Hoerr I, Von Der Muelbe P, Pascolo S;
XX DR WPI; 2003-505463/47.
XX PT Composition containing mRNA encoding tumor antigen, useful as vaccine for
XX PT treating and preventing tumors, particularly where mRNA is stabilized.
XX PS Claim 4; Page 10; 75pp; German.
XX CC This invention describes a novel pharmaceutical composition which
XX CC contains at least one polynucleotide, including at least one region that
XX CC encodes a tumour antigen and an aqueous solvent and is used for treatment
XX CC and prevention of cancer. The polynucleotide, the antigen-encoding region
XX CC and/or the 5' and/or 3'-untranslated regions are modified, relative to
XX CC the wild type, to eliminate destabilising sequences. Preferably the
XX CC polynucleotide has a 5'-cap structure and/or a polyA tail of at least 25
XX CC nucleotides, at least one internal ribosome binding site and/or at least
XX CC 5' and/or 3'-stabilising sequences. Preferably the stabilising sequences
XX CC are untranslated regions of the beta-globin gene or a sequence of formula
XX CC (C/U)CCAN x CCC(U/A)Py x UC(C/U)CC. The polynucleotide may also (i)
XX CC encode a cytokine or (ii) include a sequence that increases the
XX CC transcription rate and is complexed, or condensed, with a (poly)cationic
XX CC compound, e.g. protamine, poly(Lys or Arg) or histone. The composition
XX CC may include (i) an RNase inhibitor, especially RNasin or (ii) many
XX CC different nucleic acids, representing part of a cDNA library that encodes
XX CC tumour-specific antigens. RNA avoids problems associated with use of DNA,
XX CC e.g. integration into the genome; risk of viral recombination and
XX CC induction of anti-DNA antibodies, but is normally too unstable for
XX CC practical use. When stabilized, e.g. by incorporation of stabilizing
XX CC sequences or non-natural nucleotides, it provides an effective vaccine.
XX CC The products of the invention have cytostatic activity. This sequence
XX CC represents a sequence stabilising motif described in the disclosure of
XX CC the invention.
XX SQ Sequence 15 BP; 1 A; 8 C; 0 G; 0 T; 1 U; 5 Other;

Query Match 30.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 195
ADF29171
XX SQ Sequence 15 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 9 Other;
Query Match 30.0%; Score 3; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 10 RRR 8
|||
```

QY 4 CWW 6  
| | |  
Db 8 CWW 10

RESULT 196  
ADF29171/C  
ID ADF29171 standard; RNA; 15 BP.  
XX AC ADF29171;  
XX DT 12-FEB-2004 (revised)  
XX DT 18-SEP-2003 (first entry)  
XX DE Beta-globin stabilising RNA motif.  
XX KW tumour antigen; cancer; beta-globin; cytokine; RNase inhibitor; RNasin;  
XX KW vaccine; cytostatic; ss.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT misc\_feature 5 /tag= a  
FT /note= "Can be repeated n times where n is an undisclosed  
FT figure"  
FT misc\_feature 10 /tag= b  
FT /note= "Can be repeated n times where n is an undisclosed  
FT figure"  
XX WO2003051401-A2.  
XX 26-JUN-2003.  
XX PF 19-DEC-2002; 2002WO-EP014577.  
XX PR 19-DEC-2001; 2001DE-01062480.  
XX PA (CURE-) CUREVAC GMBH.  
XX PI Hoerr I, Von Der Muelbe F, Pascolo S;  
XX WPI; 2003-505463/47.  
XX DR Composition containing mRNA encoding tumor antigen, useful as vaccine for  
PT treating and preventing tumors, particularly where mRNA is stabilized.  
XX PS Claim 4; Page 10; 75pp; German.

CC This invention describes a novel pharmaceutical composition which  
CC contains at least one polynucleotide, including at least one region that  
CC encodes a tumour antigen and an aqueous solvent and is used for treatment  
CC and prevention of cancer. The polynucleotide, the antigen-encoding region  
CC and/or the 5' and/or 3'-untranslated regions are modified, relative to  
CC the wild type, to eliminate destabilising sequences. Preferably the  
CC polynucleotide has a 5'-cap structure and/or a polyA tail of at least 25  
CC nucleotides, at least one internal ribosome binding site and/or at least  
CC 5' and/or 3'-stabilising sequences. Preferably the stabilising sequences  
CC are untranslated regions of the beta-globin gene or a sequence of formula  
CC (C/U)CCAN x CCC(U/APY x UC(C/U)CC. The polynucleotide may also (i)  
CC encode a cytokine or (ii) include a sequence that increases the  
CC transcription rate and is complexed, or condensed, with a (poly)cationic  
CC compound, e.g. protamine, poly(Lys or Arg) or histone. The composition  
CC may include (i) an RNase inhibitor, especially RNasin or (ii) many  
CC different nucleic acids, representing part of a cDNA library that encodes  
CC tumour-specific antigens. RNA avoids problems associated with use of DNA,  
CC e.g. integration into the genome; risk of viral recombination and  
CC induction of anti-DNA antibodies, but is normally too unstable for  
CC practical use. When stabilized, e.g. by incorporation of stabilizing  
CC sequences or non-natural nucleotides, it provides an effective vaccine.  
CC The products of the invention have cytostatic activity. This sequence

CC represents a sequence stabilising motif described in the disclosure of  
CC the invention.  
XX Sequence 15 BP; 1 A; 8 C; 0 G; 0 T; 1 U; 5 Other;  
SQ

Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 WWG 7  
| | |  
Db 10 WWG 8  
| | |

RESULT 197  
ADF29180  
ID ADF29180 standard; DNA; 15 BP.  
XX AC ADF29180;  
XX DT 12-FEB-2004 (first entry)  
XX DE Binding oligonucleotide DNA #4.  
XX KW ss; library; specific-binding agent; activation; inhibition; primer.  
XX OS Synthetic.  
XX WO2003056034-A2.  
XX PD 10-JUL-2003.  
XX PF 19-DEC-2002; 2002WO-EP014584.  
XX PR 24-DEC-2001; 2001DE-01063986.  
XX PR 09-FEB-2002; 2002DE-01005423.  
XX PR 11-FEB-2002; 2002DE-01005571.  
XX PA (NANO-) NANOTYPE GMBH.  
XX PI Steipe B, Clausen-Schaumann H, Oosterhelt F;  
XX WPI; 2003-569459/53.  
XX DR In vitro selection of specific binding agents, useful potentially as  
PT pharmaceuticals and diagnostic agents, discriminates again non-specific,  
PT high-affinity agents.  
XX PS Disclosure; Fig 7; 58pp; German.

CC This invention describes a novel in vitro method for selecting agents,  
CC present in a library of molecules, that bind to a target molecule. The  
CC method comprises first immobilizing the target molecules and contacting  
CC them with many molecules, which are bound to a reference complex so that  
CC the target molecule can bind to appropriate agents, forming a link of  
CC structure reference complex-agent-target molecule. Non-bound components  
CC are separated and a force is applied to the link so that one bond in it  
CC is broken, and the target molecule-bound agent, or its complement, is  
CC identified and/or amplified. The reference complex has a binding strength  
CC chosen to be smaller than that of a specifically bound agent, when a  
CC tractive force is applied. The method is used to select specific-binding  
CC agents, potentially useful as pharmaceuticals, e.g. for activation or  
CC inhibition of targets, also for diagnosis. High-affinity but non-specific  
CC binders are not selected, rather only those with specific binding,  
CC including any present only rarely in the test population, since selection  
CC is made without reaching thermodynamic equilibrium. This results in rapid  
CC selection and does not require stringent conditions, i.e. selection  
CC conditions are similar to physiological conditions. This sequence  
CC represents an oligonucleotide used to illustrate the method of the  
CC invention.  
XX Sequence 15 BP; 7 A; 0 C; 0 G; 0 T; 0 U; 8 Other;  
SQ



Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
DB 8 RRR 10

RESULT 198  
ADF29180/C  
ID ADF29180 standard; DNA; 15 BP.

XX AC ADF29180;

XX DT 12-FEB-2004 (first entry)

XX DE Binding oligonucleotide DNA #4.

XX KW ss; library; specific-binding agent; activation; inhibition; primer.

XX OS Synthetic.

XX PN WO2003056034-A2.

XX PD 10-JUL-2003.

XX PF 19-DEC-2002; 2002WO-EP014584.

XX PR 24-DEC-2001; 2001DE-01063986.

XX PR 09-FEB-2002; 2002DE-01005423.

XX PR 11-FEB-2002; 2002DE-01005571.

XX PA (NANO-) NANOTYPE GMBH.

XX PI Steipe B, Clausen-Schaumann H, Oesterhelt F;

XX DR WPI; 2003-569459/53.

XX PT In vitro selection of specific binding agents, useful potentially as

XX PT pharmaceuticals and diagnostic agents, discriminates again non-specific,

XX PT high-affinity agents.

XX PS Disclosure; Fig 7; 58pp; German.

XX CC This invention describes a novel in vitro method for selecting agents,  
XX CC present in a library of molecules, that bind to a target molecule. The  
XX CC method comprises first immobilizing the target molecules and contacting  
XX CC them with many molecules, which are bound to a reference complex so that  
XX CC the target molecule can bind to appropriate agents, forming a link of  
XX CC structure reference complex-agent-target molecule. Non-bound components  
XX CC are separated and a force is applied to the link so that one bond in it  
XX CC is broken, and the target molecule-bound agent, or its complement, is  
XX CC identified and/or amplified. The reference complex has a binding strength  
XX CC chosen to be smaller than that of a specifically bound agent, when a  
XX CC tractive force is applied. The method is used to select specific-binding  
XX CC agents, potentially useful as pharmaceuticals, e.g. for activation or  
XX CC inhibition of targets, also for diagnosis. High-affinity but non-specific  
XX CC binders are not selected, rather only those with specific binding,  
XX CC including any present only rarely in the test population, since selection  
XX CC is made without reaching thermodynamic equilibrium. This results in rapid  
XX CC selection and does not require stringent conditions, i.e. selection  
XX CC conditions are similar to physiological conditions. This sequence  
XX CC represents an oligonucleotide used to illustrate the method of the  
XX CC invention.

XX SQ Sequence 15 BP; 7 A; 0 C; 0 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

Db 15 YYY 13  
|||

RESULT 199

ADJ71750

XX ID ADJ71750 standard; DNA; 15 BP.

XX AC ADJ71750;

XX DT 06-MAY-2004 (first entry)

XX DE Aptamer peptide display library generic insert.

XX KW cytostatic; analgesic; anticonvulsant; cerebroprotective;

XX KW antiparkinsonian; nootropic; neuroprotective; anti-HIV;

XX KW modulator of cell phenotype; gene therapy; peptide aptamer;

XX KW cell phenotype modification; peptide display library; cancer; pain;

XX KW epilepsy; stroke; Parkinson's disease; Alzheimer's disease;

XX KW Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.

XX OS Synthetic.

XX PN WO2003040168-A2.

XX PD 15-MAY-2003.

XX PF 06-NOV-2002; 2002WO-US035584.

XX PR 06-NOV-2001; 2001US-0333262P.

XX PR 14-FEB-2002; 2002US-0357278P.

XX PA (ENAN-) ENANTA PHARM INC.

XX PI Benson JD, Vincent SM, Brasher BB, Miao Z, Lamming D;

XX DR WPI; 2003-541418/51.

XX PS Example 1; SEQ ID NO 6; 173pp; English.

XX CC The invention relates to a method of identifying (M1) a peptide aptamer  
XX CC (PA) capable of modifying a cell phenotype, involving contacting a list  
XX CC sample of cells with a library of expressible nucleic acid sequences  
XX CC encoding random peptide aptamers linked to a fusion moiety, selecting at  
XX CC least one cell having an altered phenotype compared to the phenotype of  
XX CC the cell prior to contacting, and identifying peptide aptamers expressed  
XX CC in the selected cell. PA, its derivative or corresponding nucleic acid is  
XX CC useful for the molecular modelling of an agent having similar binding  
XX CC characteristics as PA. PA, its derivative or corresponding expressible  
XX CC nucleic acid is useful for treating or inhibiting a disease or condition  
XX CC (such as cancer) associated with an aberrant cell phenotype in a subject,  
XX CC where the aberrant cell phenotype is associated with a change in levels  
XX CC of apoptosis, viral resistance, signal transduction, protein trafficking,  
XX CC cell adhesion, membrane transport, cell motility, metabolic state or  
XX CC differentiation, when compared to a control cell, or the aberrant cell  
XX CC phenotype is associated with a tumor cell. The expressible nucleic acid  
XX CC is administered using a retrovirus that comprises a chromatin insulator  
XX CC element. PA is useful as a prognostic or diagnostic tool, for altering a  
XX CC cell phenotype, in gene therapy, as therapeutics for treating diseases  
XX CC (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's  
XX CC disease, Huntington's disease, multiple sclerosis, AIDS), and for the  
XX CC research and development of other therapeutics. This sequence represents  
XX CC the generic sequence used to generate the peptide display library (in  
XX CC retroviruses) and used to generate the aptamers of the invention.

XX SQ Sequence 15 BP; 3 A; 0 C; 1 G; 4 T; 0 U; 7 Other;

Query Match 30.0%; Score 3; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GY 9  
Db 11 GY 13  
RESULT 200  
ADJ71750/c  
ID ADJ71750 standard; DNA; 15 BP.  
XX AC  
XX ADJ71750;  
XX 06-MAY-2004 (first entry)  
XX DE Aptamer peptide display library generic insert.  
XX KW cytostatic; analgesic; anticonvulsant; cerebroprotective;  
KW antiparkinsonian; nootropic; neuroprotective; anti-HIV;  
KW modulator of cell phenotype; gene therapy; peptide aptamer;  
KW cell phenotype modification; peptide display library; cancer; pain;  
KW epilepsy; stroke; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.  
XX OS Synthetic.  
XX PN WO2003040168-A2.  
XX PD 15-MAY-2003.  
XX PF 06-NOV-2002; 2002WO-US035584.  
XX PR 06-NOV-2001; 2001US-0333262P.  
XX PR 14-FEB-2002; 2002US-0357278P.  
XX PA (ENAN-) ENANTA PHARM INC.  
XX PI Benson JD, Vincent SM, Brasher BB, Miao Z, Lamming D;  
XX WPI; 2003-541418/51.  
XX PT Identifying peptide aptamer capable of modifying cell phenotype, by  
XX PT contacting cell sample with library encoding random peptide aptamers,  
XX PT selecting cell with altered phenotype, and identifying aptamers expressed  
XX PS in cell.  
XX PS Example 1; SEQ ID NO 6; 173pp; English.  
XX CC The invention relates to a method of identifying (M1) a peptide aptamer  
XX CC (PA) capable of modifying a cell phenotype, involving contacting a 1st  
XX CC sample of cells with a library of expressible nucleic acid sequences  
XX CC encoding random peptide aptamers linked to a fusion moiety, selecting at  
XX CC least one cell having an altered phenotype compared to the phenotype of  
XX CC the cell prior to contacting, and identifying peptide aptamers expressed  
XX CC in the selected cell. PA, its derivative or corresponding nucleic acid is  
XX CC useful for the molecular modelling of an agent having similar binding  
XX CC characteristics as PA. PA, its derivative or corresponding expressible  
XX CC nucleic acid is useful for treating or inhibiting a disease or condition  
XX CC (such as cancer) associated with an aberrant cell phenotype in a subject,  
XX CC where the aberrant cell phenotype is associated with a change in levels  
XX CC of apoptosis, viral resistance, signal transduction, protein trafficking,  
XX CC cell adhesion, membrane transport, cell motility, metabolic state or  
XX CC differentiation, when compared to a control cell, or the aberrant cell  
XX CC phenotype is associated with a tumor cell. The expressible nucleic acid  
XX CC is administered using a retrovirus that comprises a chromatin insulator  
XX CC element. PA is useful as a prognostic or diagnostic tool, for altering a  
XX CC cell phenotype, in gene therapy, as therapeutics for treating diseases  
XX CC (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's  
XX CC disease, Huntington's disease, multiple sclerosis, AIDS), and for the  
XX CC research and development of other therapeutics. This sequence represents  
XX CC the generic sequence used to generate the peptide display library (in  
XX CC retroviruses) and used to generate the aptamers of the invention.

XX SQ Sequence 15 BP; 3 A; 0 C; 1 G; 4 T; 0 U; 7 Other;  
Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 RRC 4  
Db 13 RRC 11  
Search completed: January 14, 2005, 16:40:02  
Job time : 409 secs

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 16:22:09 ; Search time 2717 Seconds  
(without alignments)  
134.118 Million cell updates/sec

Title: US-09-813-824A-3  
Perfect score: 10  
Sequence: 1 RRRRCWGYYY 10

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 564238

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	40.0	74	CNS015BQ	AL105248 Drosophil
2	4	40.0	74	CNS015BQ	AL105248 Drosophil
3	4	40.0	77	AF211608	AF211608 AF211608
4	4	40.0	77	AF211608	AF211608 AF211608
5	3	30.0	63	AY431131	AY431131 Aedes aeg
6	3	30.0	63	AY431131	AY431131 Aedes aeg
7	3	30.0	68	CNS011MQ	AL100460 Drosophil
8	3	30.0	68	CNS011MQ	AL100460 Drosophil
9	3	30.0	70	T24836	T24836 EST411 Huma
10	3	30.0	70	T24836	T24836 EST411 Huma
11	3	30.0	88	AJ283322	AJ283322 4A3A-P8D3
12	3	30.0	88	AJ283322	AJ283322 4A3A-P8D3
13	3	30.0	90	T24971	T24971 EST546 Huma
14	3	30.0	90	T24971	T24971 EST546 Huma
15	3	30.0	91	BQ704626	BQ704626 Bn01_0312
16	3	30.0	91	BQ704626	BQ704626 Bn01_0312
17	3	30.0	92	AY431374	AY431374 Aedes aeg
18	3	30.0	93	AY431374	AY431374 Aedes aeg
19	3	30.0	93	CNS00YZ0	AL097014 Drosophil
20	3	30.0	93	CNS00YZ0	AL097014 Drosophil
21	3	30.0	96	CNS01070	AL098622 Drosophil
22	3	30.0	96	CNS01070	AL098622 Drosophil
23	3	30.0	98	CNS0429N	AL271220 Tetraodon
24	3	30.0	98	CNS0429N	AL271220 Tetraodon

C 98	2	20.0	58	3	AY439683	AY439683 Armigeres	171	2	20.0	62	9	CNS0119R	AL099993 Drosophil
C 99	2	20.0	59	1	AF211549	AF211549 Drosophil	C 172	2	20.0	62	9	CNS0119R	AL099993 Drosophil
C 100	2	20.0	59	1	AF211549	AF211549 Drosophil	C 172	2	20.0	62	9	CNS02QCA	AL209107 Tetraodon
C 101	2	20.0	59	3	AY439538	AY439538 Armigeres	C 173	2	20.0	62	9	CNS02QCA	AL209107 Tetraodon
C 102	2	20.0	59	3	AY439538	AY439538 Armigeres	C 175	2	20.0	62	9	CNS04A3J	AL281368 Tetraodon
C 103	2	20.0	59	3	CNS0111A	AL099688 Drosophil	C 176	2	20.0	62	9	CNS04A3J	AL281368 Tetraodon
C 104	2	20.0	59	9	CNS0111A	AL099688 Drosophil	C 177	2	20.0	63	2	AW444235	AW444235 AB555 Bas
C 105	2	20.0	59	9	CNS0114M	AL104200 Drosophil	C 178	2	20.0	63	2	AW444235	AW444235 AB555 Bas
C 106	2	20.0	59	9	CNS0141M	AL104200 Drosophil	C 179	2	20.0	63	2	AW444235	AW444235 AB555 Bas
C 107	2	20.0	60	2	AW059629	AW059629 HuTH.bsst	C 180	2	20.0	63	2	AW444251	AW444251 AB015 Pri
C 108	2	20.0	60	2	AW059629	AW059629 HuTH.bsst	C 181	2	20.0	63	3	AY440539	AY440539 Armigeres
C 109	2	20.0	60	2	AW582843	AW582843 top3g66 N	C 182	2	20.0	63	4	AY440539	AY440539 Armigeres
C 110	2	20.0	60	2	AW582843	AW582843 top3g66 N	C 183	2	20.0	63	4	EG838614	EG838614 Gc01_05d0
C 111	2	20.0	60	3	AY432469	AY432469 Aedes aeg	C 184	2	20.0	63	4	EG838614	EG838614 Gc01_05d0
C 112	2	20.0	60	3	AY432469	AY432469 Aedes aeg	C 185	2	20.0	63	9	CNS017GA	AL108004 Drosophil
C 113	2	20.0	60	3	AY432601	AY432601 Aedes aeg	C 186	2	20.0	63	9	CNS017GA	AL108004 Drosophil
C 114	2	20.0	60	3	AY432601	AY432601 Aedes aeg	C 187	2	20.0	63	9	CNS01VCH	AL168938 Tetraodon
C 115	2	20.0	60	9	CNS000ARA	AL055937 Drosophil	C 188	2	20.0	63	9	CNS01VCH	AL168938 Tetraodon
C 116	2	20.0	60	9	CNS000ARA	AL055937 Drosophil	C 189	2	20.0	63	9	CNS02JW3	AL200748 Tetraodon
C 117	2	20.0	60	9	CNS0101K	AL099014 Drosophil	C 190	2	20.0	63	9	CNS02JW3	AL200748 Tetraodon
C 118	2	20.0	60	9	CNS0101K	AL099014 Drosophil	C 191	2	20.0	63	9	CNS02PAK	AL207749 Tetraodon
C 119	2	20.0	60	9	CNS0115W	AL099854 Drosophil	C 192	2	20.0	63	9	CNS02PAK	AL207749 Tetraodon
C 120	2	20.0	60	9	CNS0115W	AL099854 Drosophil	C 193	2	20.0	63	9	CNS03SXE	AL259115 Tetraodon
C 121	2	20.0	60	9	CNS01TCC	AL166341 Tetraodon	C 194	2	20.0	63	9	CNS03SXE	AL259115 Tetraodon
C 122	2	20.0	60	9	CNS01TCC	AL166341 Tetraodon	C 195	2	20.0	63	9	CNS04DE2	AL285635 Tetraodon
C 123	2	20.0	60	9	CNS028B0	AL185733 Tetraodon	C 196	2	20.0	63	9	CNS04DE2	AL285635 Tetraodon
C 124	2	20.0	60	9	CNS028B0	AL185733 Tetraodon	C 197	2	20.0	64	7	R28845	R28845 F1-6D 22 we
C 125	2	20.0	60	9	CNS02K40	AL201033 Tetraodon	C 198	2	20.0	64	7	R28845	R28845 F1-6D 22 we
C 126	2	20.0	60	9	CNS02K40	AL201033 Tetraodon	C 199	2	20.0	64	9	CNS00DAF	AL060631 Drosophil
C 127	2	20.0	60	9	CNS02QD2	AL206753 Tetraodon	C 200	2	20.0	64	9	CNS00DAF	AL060631 Drosophil
C 128	2	20.0	60	9	CNS02QD2	AL206753 Tetraodon	C 201	2	20.0	64	9	CNS01122	AL100904 Drosophil
C 129	2	20.0	60	9	CNS0330M	AL225535 Tetraodon	C 202	2	20.0	64	9	CNS01122	AL100904 Drosophil
C 130	2	20.0	60	9	CNS0330M	AL225535 Tetraodon	C 203	2	20.0	64	9	CNS016S2	AL107132 Drosophil
C 131	2	20.0	60	9	CNS03C5T	AL237386 Tetraodon	C 204	2	20.0	64	9	CNS016S2	AL107132 Drosophil
C 132	2	20.0	60	9	CNS03C5T	AL237386 Tetraodon	C 205	2	20.0	64	9	CNS01WJY	AL170503 Tetraodon
C 133	2	20.0	60	9	CNS03QD2	AL255824 Tetraodon	C 206	2	20.0	64	9	CNS01WJY	AL170503 Tetraodon
C 134	2	20.0	60	9	CNS03QD2	AL255824 Tetraodon	C 207	2	20.0	64	9	CNS0263F	AL182868 Tetraodon
C 135	2	20.0	61	3	AY431565	AY431565 Aedes aeg	C 208	2	20.0	64	9	CNS0263F	AL182868 Tetraodon
C 136	2	20.0	61	3	AY431565	AY431565 Aedes aeg	C 209	2	20.0	64	9	CNS02D01	AL191835 Tetraodon
C 137	2	20.0	61	3	AY432562	AY432562 Aedes aeg	C 210	2	20.0	64	9	CNS02D01	AL191835 Tetraodon
C 138	2	20.0	61	3	AY432562	AY432562 Aedes aeg	C 211	2	20.0	64	9	CNS03NRA	AL252415 Tetraodon
C 139	2	20.0	61	3	AY432562	AY432562 Aedes aeg	C 212	2	20.0	64	9	CNS03NRA	AL252415 Tetraodon
C 140	2	20.0	61	3	AY432871	AY432871 Aedes aeg	C 213	2	20.0	65	2	AW444213	AW444213 AB501 Bas
C 141	2	20.0	61	7	L76124	L76124 SCWRAP0218	C 214	2	20.0	65	2	AW444213	AW444213 AB501 Bas
C 142	2	20.0	61	7	L76124	L76124 SCWRAP0218	C 215	2	20.0	65	3	AY439824	AY439824 Armigeres
C 143	2	20.0	61	9	CNS0139J	AL102577 Drosophil	C 216	2	20.0	65	3	AY439824	AY439824 Armigeres
C 144	2	20.0	61	9	CNS0139J	AL102577 Drosophil	C 217	2	20.0	65	9	CNS03NIN	AL252104 Tetraodon
C 145	2	20.0	61	9	CNS02U97	AL199924 Tetraodon	C 218	2	20.0	65	9	CNS03NIN	AL252104 Tetraodon
C 146	2	20.0	61	9	CNS02U97	AL199924 Tetraodon	C 219	2	20.0	66	1	AF211756	AF211756 AF211756
C 147	2	20.0	61	9	CNS02MP4	AL204385 Tetraodon	C 220	2	20.0	66	1	AF211756	AF211756 AF211756
C 148	2	20.0	61	9	CNS02MP4	AL204385 Tetraodon	C 221	2	20.0	66	1	AF211756	AF211756 AF211756
C 149	2	20.0	61	9	CNS03955	AL233474 Tetraodon	C 222	2	20.0	66	2	AW444305	AW444305 AB229 Pri
C 150	2	20.0	61	9	CNS03955	AL233474 Tetraodon	C 223	2	20.0	66	2	AW444305	AW444305 AB229 Pri
C 151	2	20.0	61	9	CNS03955	AL233474 Tetraodon	C 224	2	20.0	66	3	AY432740	AY432740 Aedes aeg
C 152	2	20.0	61	9	CNS03JDP	AL260998 Tetraodon	C 225	2	20.0	66	3	AY432740	AY432740 Aedes aeg
C 153	2	20.0	61	9	CNS044FV	AL274036 Tetraodon	C 226	2	20.0	66	7	L76130	L76130 SCWRAP0224
C 154	2	20.0	61	9	CNS044FV	AL274036 Tetraodon	C 227	2	20.0	66	9	CNS00GR8	AL072444 Drosophil
C 155	2	20.0	62	2	AW059587	AW059587 HuTH.bsst	C 228	2	20.0	66	9	CNS00GR8	AL072444 Drosophil
C 156	2	20.0	62	2	AW059587	AW059587 HuTH.bsst	C 229	2	20.0	66	9	CNS00ZKP	AL097795 Drosophil
C 157	2	20.0	62	2	AW059628	AW059628 HuTH.bsst	C 230	2	20.0	66	9	CNS00ZKP	AL097795 Drosophil
C 158	2	20.0	62	2	AW059628	AW059628 HuTH.bsst	C 231	2	20.0	66	9	CNS0212N	AL176360 Tetraodon
C 159	2	20.0	62	2	BE577741	BE577741 EST011 Pi	C 232	2	20.0	66	9	CNS0212N	AL176360 Tetraodon
C 160	2	20.0	62	2	BE577741	BE577741 EST011 Pi	C 233	2	20.0	66	9	CNS045GR	AL275364 Tetraodon
C 161	2	20.0	62	3	AY433080	AY433080 Aedes aeg	C 234	2	20.0	66	9	CNS045GR	AL275364 Tetraodon
C 162	2	20.0	62	3	AY433080	AY433080 Aedes aeg	C 235	2	20.0	67	2	AW444171	AW444171 AB308 Bas
C 163	2	20.0	62	3	AY440494	AY440494 Armigeres	C 236	2	20.0	67	2	AW444171	AW444171 AB308 Bas
C 164	2	20.0	62	3	AY440494	AY440494 Armigeres	C 237	2	20.0	67	9	CNS00AGZ	AL055768 Drosophil
C 165	2	20.0	62	5	BQ704656	BQ704656 Bn01_03h2	C 238	2	20.0	67	9	CNS00AGZ	AL055768 Drosophil
C 166	2	20.0	62	5	BQ704656	BQ704656 Bn01_03h2	C 239	2	20.0	67	9	CNS00BRW	AL057558 Drosophil
C 167	2	20.0	62	9	CNS00CEZ	AL058792 Drosophil	C 240	2	20.0	67	9	CNS00BRW	AL057558 Drosophil
C 168	2	20.0	62	9	CNS00CEZ	AL058792 Drosophil	C 241	2	20.0	67	9	CNS011DR	AL100137 Drosophil
C 169	2	20.0	62	9	CNS00IGI	AL074751 Drosophil	C 242	2	20.0	67	9	CNS011DR	AL100137 Drosophil
C 170	2	20.0	62	9	CNS00IGI	AL074751 Drosophil	C 243	2	20.0	67	9	CNS01WQ8	AL170729 Tetraodon

C 244	2	20.0	67	9	CNS01WQ8	AL170729 Tetraodon	317	2	20.0	72	7	T24492	T24492 EST067 Huma
C 245	2	20.0	67	9	CNS02O5Z	AL206288 Tetraodon	C 318	2	20.0	72	7	T24492	T24492 EST067 Huma
C 246	2	20.0	67	9	CNS02O5Z	AL206288 Tetraodon	C 319	2	20.0	72	9	CNS013KD	AL102967 Drosophil
C 247	2	20.0	67	9	CNS02PU7	AL208456 Tetraodon	C 320	2	20.0	72	9	CNS013KD	AL102967 Drosophil
C 248	2	20.0	67	9	CNS02PU7	AL208456 Tetraodon	C 321	2	20.0	72	9	CNS02411	AL180190 Tetraodon
C 249	2	20.0	67	9	CNS0482T	AL208456 Tetraodon	C 322	2	20.0	72	9	CNS02411	AL180190 Tetraodon
C 250	2	20.0	67	9	CNS0482T	AL208456 Tetraodon	C 323	2	20.0	72	9	CNS03DMN	AL239648 Tetraodon
C 251	2	20.0	67	9	CNS04KAU	AL294591 Tetraodon	C 324	2	20.0	72	9	CNS03DMN	AL239648 Tetraodon
C 252	2	20.0	67	9	CNS04KAU	AL294591 Tetraodon	C 325	2	20.0	72	9	CNS04AOG	AL282121 Tetraodon
C 253	2	20.0	68	4	BG321688	BG321688 Ds01_02h0	C 326	2	20.0	72	9	CNS04AOG	AL282121 Tetraodon
C 254	2	20.0	68	4	BG321688	BG321688 Ds01_02h0	C 327	2	20.0	73	3	AY432861	AY432861 Aedes aeg
C 255	2	20.0	68	9	CNS0010F	AL074576 Drosophil	C 328	2	20.0	73	3	AY432861	AY432861 Aedes aeg
C 256	2	20.0	68	9	CNS0010F	AL074576 Drosophil	C 329	2	20.0	73	3	AY433262	AY433262 Aedes aeg
C 257	2	20.0	68	9	CNS0115R	AL099849 Drosophil	C 330	2	20.0	73	3	AY433262	AY433262 Aedes aeg
C 258	2	20.0	68	9	CNS0115R	AL099849 Drosophil	C 331	2	20.0	73	3	AY439747	AY439747 Armigeres
C 259	2	20.0	68	9	CNS011H7	AL100261 Drosophil	C 332	2	20.0	73	3	AY439747	AY439747 Armigeres
C 260	2	20.0	68	9	CNS011H7	AL100261 Drosophil	C 333	2	20.0	73	3	AY440001	AY440001 Armigeres
C 261	2	20.0	68	9	CNS011Q8	AL100586 Drosophil	C 334	2	20.0	73	3	AY440001	AY440001 Armigeres
C 262	2	20.0	68	9	CNS011Q8	AL100586 Drosophil	C 335	2	20.0	73	3	AY440687	AY440687 Armigeres
C 263	2	20.0	68	9	CNS0223B	AL177680 Tetraodon	C 336	2	20.0	73	3	AY440687	AY440687 Armigeres
C 264	2	20.0	68	9	CNS0223B	AL177680 Tetraodon	C 337	2	20.0	73	6	CD458545	CD458545 Fg08_11h1
C 265	2	20.0	68	9	CNS02PGH	AL207962 Tetraodon	C 338	2	20.0	73	6	CD458545	CD458545 Fg08_11h1
C 266	2	20.0	68	9	CNS02PGH	AL207962 Tetraodon	C 339	2	20.0	73	9	CNS008IX	AL052135 Drosophil
C 267	2	20.0	68	9	CNS033MR	AL226332 Tetraodon	C 340	2	20.0	73	9	CNS008IX	AL052135 Drosophil
C 268	2	20.0	68	9	CNS033MR	AL226332 Tetraodon	C 341	2	20.0	73	9	CNS002Y1	AL098275 Drosophil
C 269	2	20.0	68	9	CNS04DLF	AL285900 Tetraodon	C 342	2	20.0	73	9	CNS002Y1	AL098275 Drosophil
C 270	2	20.0	68	9	CNS04DLF	AL285900 Tetraodon	C 343	2	20.0	73	9	CNS01670	AL106398 Drosophil
C 271	2	20.0	69	1	AF211775	AF211775 AF211775	C 344	2	20.0	73	9	CNS01670	AL106398 Drosophil
C 272	2	20.0	69	1	AF211775	AF211775 AF211775	C 345	2	20.0	73	9	CNS02FGM	AL195007 Tetraodon
C 273	2	20.0	69	2	AW059623	AW059623 HuTH.best	C 346	2	20.0	73	9	CNS02FGM	AL195007 Tetraodon
C 274	2	20.0	69	2	AW059623	AW059623 HuTH.best	C 347	2	20.0	73	9	CNS03MDO	AL250629 Tetraodon
C 275	2	20.0	69	2	AW059623	AW059623 HuTH.best	C 348	2	20.0	73	9	CNS03MDO	AL250629 Tetraodon
C 276	2	20.0	69	9	CNS012M7	AL101737 Drosophil	C 349	2	20.0	73	9	CNS04POB	AL301556 Tetraodon
C 277	2	20.0	69	9	CNS012M7	AL101737 Drosophil	C 350	2	20.0	73	9	CNS04POB	AL301556 Tetraodon
C 278	2	20.0	69	9	CNS015U2	AL105908 Drosophil	C 351	2	20.0	74	2	AW444240	AW444240 AB571 Bas
C 279	2	20.0	69	9	CNS015U2	AL105908 Drosophil	C 352	2	20.0	74	2	AW444240	AW444240 AB571 Bas
C 280	2	20.0	69	9	CNS0161X	AL106191 Drosophil	C 353	2	20.0	74	3	AY431853	AY431853 Aedes aeg
C 281	2	20.0	69	9	CNS0161X	AL106191 Drosophil	C 354	2	20.0	74	3	AY431853	AY431853 Aedes aeg
C 282	2	20.0	69	9	CNS01V0D	AL168502 Tetraodon	C 355	2	20.0	74	3	AY439801	AY439801 Armigeres
C 283	2	20.0	69	9	CNS01V0D	AL168502 Tetraodon	C 356	2	20.0	74	3	AY439801	AY439801 Armigeres
C 284	2	20.0	69	9	CNS03TJB	AL259904 Tetraodon	C 357	2	20.0	74	3	AY440440	AY440440 Armigeres
C 285	2	20.0	70	2	AW582796	AW582796 2zm Neuro	C 358	2	20.0	74	3	AY440440	AY440440 Armigeres
C 286	2	20.0	70	2	AW582796	AW582796 2zm Neuro	C 359	2	20.0	74	9	CNS020LX	AL175758 Tetraodon
C 287	2	20.0	70	6	CD457769	CD457769 Fg04d_030	C 360	2	20.0	74	9	CNS020LX	AL175758 Tetraodon
C 288	2	20.0	70	6	CD457769	CD457769 Fg04d_030	C 361	2	20.0	74	9	CNS02NIN	AL205448 Tetraodon
C 289	2	20.0	70	7	L76123	L76123 SCWRAP0217	C 362	2	20.0	74	9	CNS02NIN	AL205448 Tetraodon
C 290	2	20.0	70	7	L76123	L76123 SCWRAP0217	C 363	2	20.0	75	3	AY440583	AY440583 Armigeres
C 291	2	20.0	70	9	CNS01XV6	AL172203 Tetraodon	C 364	2	20.0	75	3	AY440583	AY440583 Armigeres
C 292	2	20.0	70	9	CNS01XV6	AL172203 Tetraodon	C 365	2	20.0	75	9	CNS00BGI	AL057047 Drosophil
C 293	2	20.0	70	9	CNS02E3X	AL193254 Tetraodon	C 366	2	20.0	75	9	CNS00BGI	AL057047 Drosophil
C 294	2	20.0	70	9	CNS02E3X	AL193254 Tetraodon	C 367	2	20.0	75	9	CNS00CHF	AL059284 Drosophil
C 295	2	20.0	70	9	CNS0321P	AL224268 Tetraodon	C 368	2	20.0	75	9	CNS00CHF	AL059284 Drosophil
C 296	2	20.0	70	9	CNS0321P	AL224268 Tetraodon	C 369	2	20.0	75	9	CNS03EB6	AL240171 Tetraodon
C 297	2	20.0	70	9	CNS04KX7	AL295396 Tetraodon	C 370	2	20.0	75	9	CNS03EB6	AL240171 Tetraodon
C 298	2	20.0	70	9	CNS04KX7	AL295396 Tetraodon	C 371	2	20.0	75	9	CNS048VA	AL279775 Tetraodon
C 299	2	20.0	71	2	AW059584	AW059584 HuTH.best	C 372	2	20.0	75	9	CNS048VA	AL279775 Tetraodon
C 300	2	20.0	71	2	AW059584	AW059584 HuTH.best	C 373	2	20.0	75	9	CNS06UIT	AL415899 T3 end of
C 301	2	20.0	71	3	AY439626	AY439626 Armigeres	C 374	2	20.0	75	9	CNS06UIT	AL415899 T3 end of
C 302	2	20.0	71	3	AY439626	AY439626 Armigeres	C 375	2	20.0	76	1	AF037644	AF037644 AF037644
C 303	2	20.0	71	3	AY439798	AY439798 Armigeres	C 376	2	20.0	76	1	AF037644	AF037644 AF037644
C 304	2	20.0	71	3	AY439798	AY439798 Armigeres	C 377	2	20.0	76	2	AW059546	AW059546 HuTH.best
C 305	2	20.0	71	6	CD457700	CD457700 Fg04d_03a	C 378	2	20.0	76	2	AW059546	AW059546 HuTH.best
C 306	2	20.0	71	6	CD457700	CD457700 Fg04d_03a	C 379	2	20.0	76	2	AW444223	AW444223 AB527 Bas
C 307	2	20.0	71	9	CNS002KZ	AL097805 Drosophil	C 380	2	20.0	76	2	AW444223	AW444223 AB527 Bas
C 308	2	20.0	71	9	CNS002KZ	AL097805 Drosophil	C 381	2	20.0	76	3	AY431930	AY431930 Aedes aeg
C 309	2	20.0	71	9	CNS011Z5	AL100907 Drosophil	C 382	2	20.0	76	3	AY431930	AY431930 Aedes aeg
C 310	2	20.0	71	9	CNS011Z5	AL100907 Drosophil	C 383	2	20.0	76	9	CNS004EH	AL051336 Drosophil
C 311	2	20.0	71	9	CNS01S4U	AL164775 Tetraodon	C 384	2	20.0	76	9	CNS004EH	AL051336 Drosophil
C 312	2	20.0	71	9	CNS01S4U	AL164775 Tetraodon	C 385	2	20.0	76	9	CNS02F53	AL194592 Tetraodon
C 313	2	20.0	71	9	CNS03WAK	AL263477 Tetraodon	C 386	2	20.0	76	9	CNS02F53	AL194592 Tetraodon
C 314	2	20.0	71	9	CNS03WAK	AL263477 Tetraodon	C 387	2	20.0	76	9	CNS03DSF	AL239496 Tetraodon
C 315	2	20.0	72	1	AF211718	AF211718 AF211718	C 388	2	20.0	76	9	CNS03DSF	AL239496 Tetraodon
C 316	2	20.0	72	1	AF211718	AF211718 AF211718	C 389	2	20.0	77	2	AW582791	AW582791 Imku Neur

C 390	2	20.0	77	2	AW582791	AW582791 Inku Neuro	463	2	20.0	80	9	CNS03IRP	AL245950 Tetraodon
C 391	2	20.0	77	2	AW582792	AW582792 Jjk Neuro	C 464	2	20.0	80	9	CNS03IRP	AL245950 Tetraodon
C 392	2	20.0	77	2	AW582792	AW582792 Jjk Neuro	C 465	2	20.0	80	9	CNS03V9F	AL262140 Tetraodon
C 393	2	20.0	77	3	AY433541	AY433541 Aedes aeg	C 466	2	20.0	80	9	CNS03V9F	AL262140 Tetraodon
C 394	2	20.0	77	3	AY433541	AY433541 Aedes aeg	C 467	2	20.0	81	3	AY440495	AY440495 Armigeres
C 395	2	20.0	77	3	AY440673	AY440673 Armigeres	C 468	2	20.0	81	3	AY440495	AY440495 Armigeres
C 396	2	20.0	77	3	AY440673	AY440673 Armigeres	C 469	2	20.0	81	5	BQ704805	BQ704805 Bn01_01p1
C 397	2	20.0	77	4	BG837283	BG837283 Zm10_07g0	C 470	2	20.0	81	5	BQ704805	BQ704805 Bn01_01p1
C 398	2	20.0	77	4	BG837283	BG837283 Zm10_07g0	C 471	2	20.0	81	5	BQ704805	BQ704805 Bn01_01p1
C 399	2	20.0	77	9	CNS00CSY	CNS00CSY	C 472	2	20.0	81	9	CNS01Y8M	AL172687 Tetraodon
C 400	2	20.0	77	9	CNS00CSY	CNS00CSY	C 473	2	20.0	81	9	CNS01Y8M	AL172687 Tetraodon
C 401	2	20.0	77	9	CNS00JAE	AL058467 Drosophil	C 474	2	20.0	81	9	CNS02KMP	AL201706 Tetraodon
C 402	2	20.0	77	9	CNS00JAE	AL058467 Drosophil	C 475	2	20.0	81	9	CNS02KMP	AL201706 Tetraodon
C 403	2	20.0	77	9	CNS025TN	AL076130 Drosophil	C 476	2	20.0	81	9	CNS04K3J	AL294328 Tetraodon
C 404	2	20.0	77	9	CNS025TN	AL076130 Drosophil	C 477	2	20.0	82	3	AY431186	AY431186 Aedes aeg
C 405	2	20.0	77	9	CNS030XM	AL182516 Tetraodon	C 478	2	20.0	82	3	AY431186	AY431186 Aedes aeg
C 406	2	20.0	77	9	CNS030XM	AL182516 Tetraodon	C 479	2	20.0	82	3	AY439812	AY439812 Armigeres
C 407	2	20.0	78	3	AY433574	AY433574 Aedes aeg	C 480	2	20.0	82	3	AY439812	AY439812 Armigeres
C 408	2	20.0	78	3	AY433574	AY433574 Aedes aeg	C 481	2	20.0	82	7	N84939	N84939 J1640F Huma
C 409	2	20.0	78	3	AY440042	AY440042 Armigeres	C 482	2	20.0	82	7	N84939	N84939 J1640F Huma
C 410	2	20.0	78	7	CNS52403	CNS52403 G73 Galle	C 483	2	20.0	82	9	CNS016XB	AL107321 Drosophil
C 411	2	20.0	78	7	CNS52403	CNS52403 G73 Galle	C 484	2	20.0	82	9	CNS016XB	AL107321 Drosophil
C 412	2	20.0	78	7	CNS52403	CNS52403 G73 Galle	C 485	2	20.0	82	9	CNS02514	AL182101 Tetraodon
C 413	2	20.0	78	9	CNS00EZR	AL069654 Drosophil	C 486	2	20.0	83	3	AY431468	AY431468 Aedes aeg
C 414	2	20.0	78	9	CNS00EZR	AL069654 Drosophil	C 487	2	20.0	83	3	AY431468	AY431468 Aedes aeg
C 415	2	20.0	78	9	CNS02NPX	AL205710 Tetraodon	C 488	2	20.0	83	3	AY431573	AY431573 Aedes aeg
C 416	2	20.0	78	9	CNS02NPX	AL205710 Tetraodon	C 489	2	20.0	83	3	AY431573	AY431573 Aedes aeg
C 417	2	20.0	78	9	CNS03193	AL223248 Tetraodon	C 490	2	20.0	83	3	AY433590	AY433590 Aedes aeg
C 418	2	20.0	78	9	CNS03193	AL223248 Tetraodon	C 491	2	20.0	83	3	AY433590	AY433590 Aedes aeg
C 419	2	20.0	78	9	CNS03B4L	AL236046 Tetraodon	C 492	2	20.0	83	7	T24924	T24924 EST499 Huma
C 420	2	20.0	78	9	CNS03B4L	AL236046 Tetraodon	C 493	2	20.0	83	7	T24924	T24924 EST499 Huma
C 421	2	20.0	78	9	CNS03FSU	AL242103 Tetraodon	C 494	2	20.0	83	7	T24924	T24924 EST499 Huma
C 422	2	20.0	78	9	CNS03FSU	AL242103 Tetraodon	C 495	2	20.0	83	9	CNS02D56	AL192003 Tetraodon
C 423	2	20.0	78	9	CNS03FUA	AL242149 Tetraodon	C 496	2	20.0	83	9	CNS02D56	AL192003 Tetraodon
C 424	2	20.0	78	9	CNS03FUA	AL242149 Tetraodon	C 497	2	20.0	83	9	CNS03BUA	AL236575 Tetraodon
C 425	2	20.0	78	9	CNS044A0	AL273825 Tetraodon	C 498	2	20.0	83	9	CNS03BUA	AL236575 Tetraodon
C 426	2	20.0	78	9	CNS044A0	AL273825 Tetraodon	C 499	2	20.0	83	9	CNS03KK9	AL255122 Tetraodon
C 427	2	20.0	78	9	CNS04DFE	AL285684 Tetraodon	C 500	2	20.0	84	3	AY431112	AY431112 Aedes aeg
C 428	2	20.0	78	9	CNS04DFE	AL285684 Tetraodon	C 501	2	20.0	84	3	AY431112	AY431112 Aedes aeg
C 429	2	20.0	79	6	CD457690	CD457690 Fg04d_03a	C 502	2	20.0	84	3	AY431112	AY431112 Aedes aeg
C 430	2	20.0	79	6	CD457690	CD457690 Fg04d_03a	C 503	2	20.0	84	3	AY431112	AY431112 Aedes aeg
C 431	2	20.0	79	9	CNS003KM	AL064929 Drosophil	C 504	2	20.0	84	3	AY431195	AY431195 Aedes aeg
C 432	2	20.0	79	9	CNS003KM	AL064929 Drosophil	C 505	2	20.0	84	3	AY431195	AY431195 Aedes aeg
C 433	2	20.0	79	9	CNS0066J	AL062856 Drosophil	C 506	2	20.0	84	3	AY440433	AY440433 Armigeres
C 434	2	20.0	79	9	CNS0066J	AL062856 Drosophil	C 507	2	20.0	84	3	AY440433	AY440433 Armigeres
C 435	2	20.0	79	9	CNS00A61	AL054768 Drosophil	C 508	2	20.0	84	9	CNS02KB5	AL201290 Tetraodon
C 436	2	20.0	79	9	CNS00A61	AL054768 Drosophil	C 509	2	20.0	84	9	CNS02QJF	AL201290 Tetraodon
C 437	2	20.0	79	9	CNS02F6H	AL194642 Tetraodon	C 510	2	20.0	84	9	CNS02QJF	AL201290 Tetraodon
C 438	2	20.0	79	9	CNS02F6H	AL194642 Tetraodon	C 511	2	20.0	84	9	CNS03VJT	AL209368 Tetraodon
C 439	2	20.0	79	9	CNS0304M	AL252895 Tetraodon	C 512	2	20.0	84	9	CNS03VJT	AL209368 Tetraodon
C 440	2	20.0	79	9	CNS0304M	AL252895 Tetraodon	C 513	2	20.0	84	9	CNS03VJT	AL209368 Tetraodon
C 441	2	20.0	79	9	CNS03P67	AL254248 Tetraodon	C 514	2	20.0	84	9	CNS03Z16	AL262514 Tetraodon
C 442	2	20.0	79	9	CNS03P67	AL254248 Tetraodon	C 515	2	20.0	84	9	CNS03Z16	AL262514 Tetraodon
C 443	2	20.0	79	9	CNS03UKX	AL261258 Tetraodon	C 516	2	20.0	84	9	CNS041NL	AL267639 Tetraodon
C 444	2	20.0	79	9	CNS03UKX	AL261258 Tetraodon	C 517	2	20.0	84	9	CNS041NL	AL267639 Tetraodon
C 445	2	20.0	79	9	CNS045UN	AL261258 Tetraodon	C 518	2	20.0	84	9	CNS04MNO	AL270426 Tetraodon
C 446	2	20.0	79	9	CNS045UN	AL261258 Tetraodon	C 519	2	20.0	84	9	CNS04MNO	AL270426 Tetraodon
C 447	2	20.0	79	9	CNS04GVO	AL290157 Tetraodon	C 520	2	20.0	85	1	AF211809	AL297645 Tetraodon
C 448	2	20.0	79	9	CNS04GVO	AL290157 Tetraodon	C 521	2	20.0	85	1	AF211809	AL297645 Tetraodon
C 449	2	20.0	80	1	AF211579	AF211579	C 522	2	20.0	85	3	AY433048	AY433048 Aedes aeg
C 450	2	20.0	80	1	AF211579	AF211579	C 523	2	20.0	85	3	AY433048	AY433048 Aedes aeg
C 451	2	20.0	80	3	AY439823	AY439823 Armigeres	C 524	2	20.0	85	3	AY440490	AY440490 Armigeres
C 452	2	20.0	80	3	AY439823	AY439823 Armigeres	C 525	2	20.0	85	3	AY440490	AY440490 Armigeres
C 453	2	20.0	80	5	BU238494	BU238494 Dg01_15c0	C 526	2	20.0	85	9	CNS02EGF	AL193704 Tetraodon
C 454	2	20.0	80	5	BU238494	BU238494 Dg01_15c0	C 527	2	20.0	85	9	CNS02EGF	AL193704 Tetraodon
C 455	2	20.0	80	7	N55635	N55635 ESTG183 Rat	C 528	2	20.0	85	9	CNS03A1F	AL234636 Tetraodon
C 456	2	20.0	80	7	N55635	N55635 ESTG183 Rat	C 529	2	20.0	85	9	CNS03A1F	AL234636 Tetraodon
C 457	2	20.0	80	9	CNS01YGN	AL172976 Tetraodon	C 530	2	20.0	85	9	CNS03NFO	AL251373 Tetraodon
C 458	2	20.0	80	9	CNS01YGN	AL172976 Tetraodon	C 531	2	20.0	85	9	CNS03NFO	AL251373 Tetraodon
C 459	2	20.0	80	9	CNS02JQ4	AL200533 Tetraodon	C 532	2	20.0	85	9	CNS04MB8	AL297197 Tetraodon
C 460	2	20.0	80	9	CNS02JQ4	AL200533 Tetraodon	C 533	2	20.0	86	3	AY439581	AY439581 Armigeres
C 461	2	20.0	80	9	CNS02LRO	AL203181 Tetraodon	C 534	2	20.0	86	3	AY439581	AY439581 Armigeres
C 462	2	20.0	80	9	CNS02LRO	AL203181 Tetraodon	C 535	2	20.0	86	3	AY440481	AY440481 Armigeres

c 536	2	20.0	86	3	AY440481	AY440481	Armigeres	609	2	20.0	89	9	CNS04G20	AL289113	Tetraodon
c 537	2	20.0	86	9	CNS00GV1	AL072689	Drosophil	c 610	2	20.0	89	9	CNS04G20	AL289113	Tetraodon
c 538	2	20.0	86	9	CNS00GV1	AL072689	Drosophil	c 611	2	20.0	89	9	CNS04J97	AL293236	Tetraodon
c 539	2	20.0	86	9	CNS01SSB	AL165620	Tetraodon	c 612	2	20.0	89	9	CNS04J97	AL293236	Tetraodon
c 540	2	20.0	86	9	CNS01SSB	AL165620	Tetraodon	c 613	2	20.0	90	2	AW582788	AW582788	2rhC Neur
c 541	2	20.0	86	9	CNS021IJ	AL176932	Tetraodon	c 614	2	20.0	90	2	AW582788	AW582788	2rhC Neur
c 542	2	20.0	86	9	CNS021IJ	AL176932	Tetraodon	c 615	2	20.0	90	2	CNS010K9	AL099075	Drosophil
c 543	2	20.0	86	9	CNS02FGJ	AL195004	Tetraodon	c 616	2	20.0	90	9	CNS010K9	AL099075	Drosophil
c 544	2	20.0	86	9	CNS02FGJ	AL195004	Tetraodon	c 617	2	20.0	90	9	CNS03ROA	AL235459	Tetraodon
c 545	2	20.0	86	9	CNS02PYH	AL208610	Tetraodon	c 618	2	20.0	90	9	CNS03ROA	AL235459	Tetraodon
c 546	2	20.0	86	9	CNS02PYH	AL208610	Tetraodon	c 619	2	20.0	90	9	CNS03X7V	AL264676	Tetraodon
c 547	2	20.0	86	9	CNS03NLI	AL252207	Tetraodon	c 620	2	20.0	90	9	CNS03X7V	AL264676	Tetraodon
c 548	2	20.0	86	9	CNS03NLI	AL252207	Tetraodon	c 621	2	20.0	91	2	AW455211	AW455211	1rk Neuro
c 549	2	20.0	86	9	CNS04GPP	AL289942	Tetraodon	c 622	2	20.0	91	2	AW455211	AW455211	1rk Neuro
c 550	2	20.0	86	9	CNS04GPP	AL289942	Tetraodon	c 623	2	20.0	91	3	AY431378	AY431378	Aedes aeg
c 551	2	20.0	86	9	CNS04JXY	AL294127	Tetraodon	c 624	2	20.0	91	3	AY431378	AY431378	Aedes aeg
c 552	2	20.0	86	9	CNS04JXY	AL294127	Tetraodon	c 625	2	20.0	91	3	AY440500	AY440500	Armigeres
c 553	2	20.0	86	9	CNS04LIP	AL296170	Tetraodon	c 626	2	20.0	91	3	AY440500	AY440500	Armigeres
c 554	2	20.0	86	9	CNS04LIP	AL296170	Tetraodon	c 627	2	20.0	91	7	CNS13428	CNS13428	FG06_07a0
c 555	2	20.0	87	1	AA231948	AA231948	AS31SB003	c 628	2	20.0	91	7	CNS13428	CNS13428	FG06_07a0
c 556	2	20.0	87	1	AA231948	AA231948	AS31SB003	c 629	2	20.0	91	7	L46987	L46987	SCMRAP074 C
c 557	2	20.0	87	2	AW444385	AW444385	AB513 Pri	c 630	2	20.0	91	7	L46987	L46987	SCMRAP074 C
c 558	2	20.0	87	2	AW444385	AW444385	AB513 Pri	c 631	2	20.0	91	9	CNS02TFY	AL213127	Tetraodon
c 559	2	20.0	87	3	AY433208	AY433208	Aedes aeg	c 632	2	20.0	91	9	CNS02TFY	AL213127	Tetraodon
c 560	2	20.0	87	3	AY433208	AY433208	Aedes aeg	c 633	2	20.0	91	9	CNS03BVX	AL237030	Tetraodon
c 561	2	20.0	87	3	AY433366	AY433366	Aedes aeg	c 634	2	20.0	91	9	CNS03BVX	AL237030	Tetraodon
c 562	2	20.0	87	3	AY433366	AY433366	Aedes aeg	c 635	2	20.0	92	1	AJ283197	AJ283197	4A3A-P7H1
c 563	2	20.0	87	9	CNS0011T	AL074323	Drosophil	c 636	2	20.0	92	1	AJ283197	AJ283197	4A3A-P7H1
c 564	2	20.0	87	9	CNS0011T	AL074323	Drosophil	c 637	2	20.0	92	2	AW059583	AW059583	HUTH.bsst
c 565	2	20.0	87	9	CNS012UH	AL102035	Drosophil	c 638	2	20.0	92	2	AW059583	AW059583	HUTH.bsst
c 566	2	20.0	87	9	CNS012UH	AL102035	Drosophil	c 639	2	20.0	92	3	AY432337	AY432337	Aedes aeg
c 567	2	20.0	87	9	CNS012BQ	AL174095	Tetraodon	c 640	2	20.0	92	3	AY432337	AY432337	Aedes aeg
c 568	2	20.0	87	9	CNS012BQ	AL174095	Tetraodon	c 641	2	20.0	92	7	L46963	L46963	SCMRAP050 C
c 569	2	20.0	87	9	CNS0238Y	AL179179	Tetraodon	c 642	2	20.0	92	7	L46963	L46963	SCMRAP050 C
c 570	2	20.0	87	9	CNS0238Y	AL179179	Tetraodon	c 643	2	20.0	92	7	T25154	T25154	EST729 Huma
c 571	2	20.0	87	9	CNS02VPL	AL216066	Tetraodon	c 644	2	20.0	92	7	T25154	T25154	EST729 Huma
c 572	2	20.0	87	9	CNS02VPL	AL216066	Tetraodon	c 645	2	20.0	92	9	CNS005AX	AL057857	Drosophil
c 573	2	20.0	87	9	CNS03KZC	AL248817	Tetraodon	c 646	2	20.0	92	9	CNS005AX	AL057857	Drosophil
c 574	2	20.0	87	9	CNS03KZC	AL248817	Tetraodon	c 647	2	20.0	92	9	CNS011DU	AL100140	Drosophil
c 575	2	20.0	87	9	CNS04AS9	AL282258	Tetraodon	c 648	2	20.0	92	9	CNS011DU	AL100140	Drosophil
c 576	2	20.0	87	9	CNS04AS9	AL282258	Tetraodon	c 649	2	20.0	93	1	AF211665	AF211665	AF211665
c 577	2	20.0	87	9	CNS04PIX	AL300750	Tetraodon	c 650	2	20.0	93	1	AF211665	AF211665	AF211665
c 578	2	20.0	87	9	CNS04PIX	AL300750	Tetraodon	c 651	2	20.0	93	2	BE217190	BE217190	2008AEDM
c 579	2	20.0	87	9	CNS04PIX	AL301348	Tetraodon	c 652	2	20.0	93	2	BE217190	BE217190	2008AEDM
c 580	2	20.0	87	9	CNS04PIJ	AL301348	Tetraodon	c 653	2	20.0	93	3	AY439491	AY439491	Armigeres
c 581	2	20.0	87	9	CNS04PIJ	AL301348	Tetraodon	c 654	2	20.0	93	3	AY439491	AY439491	Armigeres
c 582	2	20.0	88	2	AW444353	AW444353	AB428 Pri	c 655	2	20.0	93	3	AY440370	AY440370	Armigeres
c 583	2	20.0	88	3	AY440693	AY440693	Armigeres	c 656	2	20.0	93	3	AY440370	AY440370	Armigeres
c 584	2	20.0	88	3	AY440693	AY440693	Armigeres	c 657	2	20.0	93	3	AY441413	AY441413	Armigeres
c 585	2	20.0	88	9	CNS0046A	AL066315	Drosophil	c 658	2	20.0	93	3	AY441413	AY441413	Armigeres
c 586	2	20.0	88	9	CNS0046A	AL066315	Drosophil	c 659	2	20.0	93	9	CNS00795	AL066670	Drosophil
c 587	2	20.0	88	9	CNS02PXH	AL195614	Tetraodon	c 660	2	20.0	93	9	CNS00795	AL066670	Drosophil
c 588	2	20.0	88	9	CNS02PXH	AL195614	Tetraodon	c 661	2	20.0	93	9	CNS00ZCN	AL097505	Drosophil
c 589	2	20.0	88	9	CNS02GFS	AL196273	Tetraodon	c 662	2	20.0	93	9	CNS00ZCN	AL097505	Drosophil
c 590	2	20.0	88	9	CNS02GFS	AL196273	Tetraodon	c 663	2	20.0	93	9	CNS01710	AL107478	Drosophil
c 591	2	20.0	89	3	AY440689	AY440689	Armigeres	c 664	2	20.0	93	9	CNS01710	AL107478	Drosophil
c 592	2	20.0	89	3	AY440689	AY440689	Armigeres	c 665	2	20.0	93	9	CNS01710	AL107478	Drosophil
c 593	2	20.0	89	6	CB686411	CB686411	Bn01b_04h	c 666	2	20.0	93	9	CNS01T1X	AL165966	Tetraodon
c 594	2	20.0	89	6	CB686411	CB686411	Bn01b_04h	c 667	2	20.0	93	9	CNS01T1X	AL165966	Tetraodon
c 595	2	20.0	89	8	AF219015	AF219015	AF219015	c 668	2	20.0	93	9	CNS029BF	AL187044	Tetraodon
c 596	2	20.0	89	8	AF219015	AF219015	AF219015	c 669	2	20.0	93	9	CNS029BF	AL187044	Tetraodon
c 597	2	20.0	89	9	CNS00JC6	AL075992	Drosophil	c 670	2	20.0	93	9	CNS03FPU	AL241707	Tetraodon
c 598	2	20.0	89	9	CNS00JC6	AL075992	Drosophil	c 671	2	20.0	93	9	CNS03FPU	AL241707	Tetraodon
c 599	2	20.0	89	9	CNS01YJC	AL173073	Tetraodon	c 672	2	20.0	93	9	CNS03IFL	AL245514	Tetraodon
c 600	2	20.0	89	9	CNS01YJC	AL173073	Tetraodon	c 673	2	20.0	93	9	CNS03IFL	AL245514	Tetraodon
c 601	2	20.0	89	9	CNS025K1	AL182170	Tetraodon	c 674	2	20.0	93	9	CNS03WVC	AL264261	Tetraodon
c 602	2	20.0	89	9	CNS025K1	AL182170	Tetraodon	c 675	2	20.0	94	2	AW444177	AW444177	AB320 Bas
c 603	2	20.0	89	9	CNS02NCV	AL205240	Tetraodon	c 676	2	20.0	94	2	AW444177	AW444177	AB320 Bas
c 604	2	20.0	89	9	CNS02NCV	AL205240	Tetraodon	c 677	2	20.0	94	6	CD457338	CD457338	FG05_02m1
c 605	2	20.0	89	9	CNS03QOZ	AL209564	Tetraodon	c 678	2	20.0	94	6	CD457338	CD457338	FG05_02m1
c 606	2	20.0	89	9	CNS03QOZ	AL209564	Tetraodon	c 679	2	20.0	94	9	CNS0081Y	AL052136	Drosophil
c 607	2	20.0	89	9	CNS03DTD	AL239530	Tetraodon	c 680	2	20.0	94	9	CNS0081Y	AL052136	Drosophil
c 608	2	20.0	89	9	CNS03DTD	AL239530	Tetraodon	c 681	2	20.0	94	9	CNS011G8	AL100226	Drosophil

c 682	2	20.0	94	9	CNS011G8	AL100226 Drosophil	755	2	20.0	99	3	AY431446	AY431446 Aedes aeg
c 683	2	20.0	94	9	CNS0170X	AL107451 Drosophil	c 756	2	20.0	99	3	AY431446	AY431446 Aedes aeg
c 684	2	20.0	94	9	CNS0170X	AL107451 Drosophil	c 757	2	20.0	99	3	AY431503	AY431503 Aedes aeg
c 685	2	20.0	94	9	CNS02QIM	AL209335 Tetraodon	c 758	2	20.0	99	3	AY431503	AY431503 Aedes aeg
c 686	2	20.0	94	9	CNS02QIM	AL209335 Tetraodon	c 759	2	20.0	99	3	AY432126	AY432126 Aedes aeg
c 687	2	20.0	95	1	AI001441	AI001441 EST0022 T	c 760	2	20.0	99	3	AY432126	AY432126 Aedes aeg
c 688	2	20.0	95	1	AI001441	AI001441 EST0022 T	c 761	2	20.0	99	3	AY432126	AY432126 Aedes aeg
c 689	2	20.0	95	2	AW497636	AW497636 RPS20G5B8	c 762	2	20.0	99	9	CNS004DR	AL051310 Drosophil
c 690	2	20.0	95	2	AW497636	AW497636 RPS20G5B8	c 763	2	20.0	99	9	CNS004DR	AL051310 Drosophil
c 691	2	20.0	95	2	AW621134	AW621134 2ji Neuro	c 764	2	20.0	99	9	CNS027LM	AL184819 Tetraodon
c 692	2	20.0	95	2	AW621134	AW621134 2ji Neuro	c 765	2	20.0	99	9	CNS027LM	AL184819 Tetraodon
c 693	2	20.0	95	3	AY440569	AY440569 Armigeres	c 766	2	20.0	99	9	CNS036R8	AL230381 Tetraodon
c 694	2	20.0	95	3	AY440569	AY440569 Armigeres	c 767	2	20.0	99	9	CNS036R8	AL230381 Tetraodon
c 695	2	20.0	95	6	CD649674	CD649674 Cvg110037	c 768	2	20.0	99	9	CNS03AEJ	AL233108 Tetraodon
c 696	2	20.0	95	6	CD649674	CD649674 Cvg110037	c 769	2	20.0	99	9	CNS06ULL	AL415999 T7 end of
c 697	2	20.0	95	9	CNS025GK	AL182045 Tetraodon	c 770	2	20.0	99	9	CNS06ULL	AL415999 T7 end of
c 698	2	20.0	95	9	CNS025GK	AL182045 Tetraodon	c 771	2	20.0	100	1	AI617502	AI617502 zehni1689.
c 699	2	20.0	95	9	CNS02OR2	AL207047 Tetraodon	c 772	2	20.0	100	1	AI617502	AI617502 zehni1689.
c 700	2	20.0	95	9	CNS02OR2	AL207047 Tetraodon	c 773	2	20.0	100	2	AW621120	AW621120 ERAD3924
c 701	2	20.0	95	9	CNS02RN5	AL210794 Tetraodon	c 774	2	20.0	100	2	AW621120	AW621120 ERAD3924
c 702	2	20.0	95	9	CNS02RN5	AL210794 Tetraodon	c 775	2	20.0	100	2	AW621120	AW621120 ERAD3924
c 703	2	20.0	95	9	CNS03WCO	AL263553 Tetraodon	c 776	2	20.0	100	3	AY431923	AY431923 Aedes aeg
c 704	2	20.0	95	9	CNS03WCO	AL263553 Tetraodon	c 777	2	20.0	100	3	AY431923	AY431923 Aedes aeg
c 705	2	20.0	96	3	AY432683	AY432683 Aedes aeg	c 778	2	20.0	100	3	AY432099	AY432099 Aedes aeg
c 706	2	20.0	96	3	AY432683	AY432683 Aedes aeg	c 779	2	20.0	100	3	AY432099	AY432099 Aedes aeg
c 707	2	20.0	96	3	AY439832	AY439832 Armigeres	c 780	2	20.0	100	3	AY440198	AY440198 Armigeres
c 708	2	20.0	96	3	AY439832	AY439832 Armigeres	c 781	2	20.0	100	5	BQ640980	BQ640980 SSH-Bbblc
c 709	2	20.0	96	3	AY440135	AY440135 Armigeres	c 782	2	20.0	100	5	BQ640980	BQ640980 SSH-Bbblc
c 710	2	20.0	96	3	AY440135	AY440135 Armigeres	c 783	2	20.0	100	9	CNS00CGH	AL059250 Drosophil
c 711	2	20.0	96	7	L76125	L76125 SCMRAP0219	c 784	2	20.0	100	9	CNS00CGH	AL059250 Drosophil
c 712	2	20.0	96	7	L76125	L76125 SCMRAP0219	c 785	2	20.0	100	9	CNS03SM2	AL258707 Tetraodon
c 713	2	20.0	96	9	CNS01136	AL099756 Drosophil	c 786	2	20.0	100	9	CNS03SM2	AL258707 Tetraodon
c 714	2	20.0	96	9	CNS01136	AL099756 Drosophil	c 787	2	20.0	100	9	CNS06UXS	AL416438 T7 end of
c 715	2	20.0	96	9	CNS011NO	AL100470 Drosophil	c 788	2	20.0	100	9	CNS06UXS	AL416438 T7 end of
c 716	2	20.0	96	9	CNS011NO	AL100470 Drosophil	c 789	1	10.0	2	1	AL039341	AL039341 DKFZp434F
c 717	2	20.0	96	9	CNS02RIG	AL210013 Tetraodon	c 790	1	10.0	2	1	AL039341	AL039341 DKFZp434F
c 718	2	20.0	96	9	CNS02RIG	AL210013 Tetraodon	c 791	1	10.0	2	1	AL042337	AL042337 DKFZp434O
c 719	2	20.0	97	1	AF211555	AF211555 AF211555	c 792	1	10.0	2	1	AL042337	AL042337 DKFZp434O
c 720	2	20.0	97	1	AF211555	AF211555 AF211555	c 793	1	10.0	2	1	AL043859	AL043859 DKFZp434B
c 721	2	20.0	97	1	AF282937	AJ782937 4A3A-P2A1	c 794	1	10.0	2	1	AL043859	AL043859 DKFZp434B
c 722	2	20.0	97	1	AJ782937	AJ782937 4A3A-P2A1	c 795	1	10.0	2	1	AL047069	AL047069 DKFZp586P
c 723	2	20.0	97	1	AJ782937	AJ782937 4A3A-P2A1	c 796	1	10.0	2	1	AL047069	AL047069 DKFZp586P
c 724	2	20.0	97	2	AW059611	AW059611 HuTH.best	c 797	1	10.0	2	5	BX266185	BX266185 BX266185
c 725	2	20.0	97	2	AW059611	AW059611 HuTH.best	c 798	1	10.0	2	5	BX266185	BX266185 BX266185
c 726	2	20.0	97	3	AY439456	AY439456 Armigeres	c 799	1	10.0	2	5	BX266185	BX266185 BX266185
c 727	2	20.0	97	3	AY439456	AY439456 Armigeres	c 800	1	10.0	2	5	BX266563	BX266563 BX266563
c 728	2	20.0	97	3	CNS010GZ	AL098957 Drosophil	c 801	1	10.0	2	5	BX267110	BX267110 BX267110
c 729	2	20.0	97	9	CNS010GZ	AL098957 Drosophil	c 802	1	10.0	2	5	BX267110	BX267110 BX267110
c 730	2	20.0	97	9	CNS01YLD	AL173146 Tetraodon	c 803	1	10.0	2	5	BX267110	BX267110 BX267110
c 731	2	20.0	97	9	CNS01YLD	AL173146 Tetraodon	c 804	1	10.0	2	5	BX267110	BX267110 BX267110
c 732	2	20.0	97	9	CNS02DF1	AL192375 Tetraodon	c 805	1	10.0	2	6	CAS50819	CAS50819 D06H04_HO
c 733	2	20.0	97	9	CNS02DF1	AL192375 Tetraodon	c 806	1	10.0	2	6	CAS50819	CAS50819 D06H04_HO
c 734	2	20.0	97	9	CNS02VKN	AL216356 Tetraodon	c 807	1	10.0	2	6	CAS50842	CAS50842 D07B06_C1
c 735	2	20.0	97	9	CNS03B08	AL233889 Tetraodon	c 808	1	10.0	2	6	CAS50842	CAS50842 D07B06_C1
c 736	2	20.0	97	9	CNS03B08	AL233889 Tetraodon	c 809	1	10.0	2	6	CAS51273	CAS51273 D12A01_B1
c 737	2	20.0	97	9	CNS03B08	AL233889 Tetraodon	c 810	1	10.0	2	6	CAS51273	CAS51273 D12A01_B1
c 738	2	20.0	97	9	CNS03BEK	AL236405 Tetraodon	c 811	1	10.0	2	6	CF280384	CF280384 14ETL--07
c 739	2	20.0	97	9	CNS03BEK	AL236405 Tetraodon	c 812	1	10.0	2	6	CF280384	CF280384 14ETL--07
c 740	2	20.0	97	9	CNS03D3H	AL238598 Tetraodon	c 813	1	10.0	2	6	CF280384	CF280384 14ETL--07
c 741	2	20.0	98	2	AW466364	AW466364 gh59a7b27	c 814	1	10.0	2	6	CF280511	CF280511 14ETL--07
c 742	2	20.0	98	2	AW466364	AW466364 gh59a7b27	c 815	1	10.0	2	6	CF280511	CF280511 14ETL--07
c 743	2	20.0	98	3	AY431591	AY431591 Aedes aeg	c 816	1	10.0	2	6	CF281609	CF281609 14ETL--08
c 744	2	20.0	98	3	AY431591	AY431591 Aedes aeg	c 817	1	10.0	2	6	CF281609	CF281609 14ETL--08
c 745	2	20.0	98	3	AY433487	AY433487 Aedes aeg	c 818	1	10.0	2	6	CF291112	CF291112 14ROOT--0
c 746	2	20.0	98	3	AY433487	AY433487 Aedes aeg	c 819	1	10.0	2	6	CF291112	CF291112 14ROOT--0
c 747	2	20.0	98	7	CNS11517	CNS11517 Fg13_01m2	c 820	1	10.0	2	6	CF299550	CF299550 7LEAF--03
c 748	2	20.0	98	7	CNS11517	CNS11517 Fg13_01m2	c 821	1	10.0	2	6	CF299550	CF299550 7LEAF--03
c 749	2	20.0	98	9	CNS00CKL	AL059196 Drosophil	c 822	1	10.0	2	6	CF299820	CF299820 7LEAF--03
c 750	2	20.0	98	9	CNS00CKL	AL059196 Drosophil	c 823	1	10.0	2	6	CF299820	CF299820 7LEAF--03
c 751	2	20.0	98	9	CNS00IF3	AL074381 Drosophil	c 824	1	10.0	2	6	CF301411	CF301411 7LEAF--06
c 752	2	20.0	98	9	CNS00IF3	AL074381 Drosophil	c 825	1	10.0	2	6	CF301411	CF301411 7LEAF--06
c 753	2	20.0	98	9	CNS04PYV	AL301936 Tetraodon	c 826	1	10.0	2	6	CF306288	CF306288 HDAL--03
c 754	2	20.0	98	9	CNS04PYV	AL301936 Tetraodon	c 827	1	10.0	2	6	CF306288	CF306288 HDAL--03



C 828	1	10.0	2	6	CF307078	CF307078	HDAL--05-	901	1	10.0	3	6	CA851961	D19E06_I1
C 829	1	10.0	2	6	CF307123	CF307123	HDAL--05-	C 902	1	10.0	3	6	CA851961	D19E06_I1
C 830	1	10.0	2	6	CF307123	CF307123	HDAL--05-	903	1	10.0	3	6	CF282217	14E7L--09
C 831	1	10.0	2	6	CF307878	CF307878	ABF--01-H	C 904	1	10.0	3	6	CF282217	14E7L--09
C 832	1	10.0	2	6	CF307878	CF307878	ABF--01-H	905	1	10.0	3	6	CF292073	14ROOT--0
C 833	1	10.0	2	6	CF311389	CF311389	ABF--06-J	C 906	1	10.0	3	6	CF292073	14ROOT--0
C 834	1	10.0	2	6	CF311389	CF311389	ABF--06-J	907	1	10.0	3	6	CF296126	30DGS--06
C 835	1	10.0	2	6	CF311851	CF311851	ABF--07-E	C 908	1	10.0	3	6	CF296126	30DGS--06
C 836	1	10.0	2	6	CF311851	CF311851	ABF--07-E	909	1	10.0	3	6	CF299282	7LEAF--03
C 837	1	10.0	2	6	CF3115237	CF3115237	HD--04-B0	C 910	1	10.0	3	6	CF299282	7LEAF--03
C 838	1	10.0	2	6	CF315237	CF315237	HD--04-B0	911	1	10.0	3	6	CF300120	7LEAF--04
C 839	1	10.0	2	6	CF329006	CF329006	NACL--04-	C 912	1	10.0	3	6	CF300120	7LEAF--04
C 840	1	10.0	2	6	CF329006	CF329006	NACL--04-	913	1	10.0	3	6	CF302599	7LEAF--08
C 841	1	10.0	2	6	CF331310	CF331310	NACL--07-	C 914	1	10.0	3	6	CF302599	7LEAF--08
C 842	1	10.0	2	6	CF331310	CF331310	NACL--07-	915	1	10.0	3	6	CF305942	HDAL--02-
C 843	1	10.0	2	6	CF333014	CF333014	JMT--01-L	C 916	1	10.0	3	6	CF305942	HDAL--02-
C 844	1	10.0	2	6	CF333014	CF333014	JMT--01-L	917	1	10.0	3	6	CF306332	HDAL--03-
C 845	1	10.0	2	6	CF340219	CF340219	RCL1--07-	C 918	1	10.0	3	6	CF306332	HDAL--03-
C 846	1	10.0	2	6	CF340219	CF340219	RCL1--07-	919	1	10.0	3	6	CF306493	HDAL--04-
C 847	1	10.0	2	7	CK632229	CK632229	AML--AM000	C 920	1	10.0	3	6	CF306493	HDAL--04-
C 848	1	10.0	2	7	CK632229	CK632229	AML--AM000	921	1	10.0	3	6	CF306655	HDAL--04-
C 849	1	10.0	2	7	CK632229	CK632229	AML--AM000	C 922	1	10.0	3	6	CF306655	HDAL--04-
C 850	1	10.0	2	7	CK632229	CK632229	AML--AM000	923	1	10.0	3	6	CF306732	HDAL--04-
C 851	1	10.0	2	7	CK632229	CK632229	AML--AM000	C 924	1	10.0	3	6	CF306732	HDAL--04-
C 852	1	10.0	2	7	CK632229	CK632229	AML--AM000	925	1	10.0	3	6	CF306759	HDAL--04-
C 853	1	10.0	2	7	CK632229	CK632229	AML--AM000	C 926	1	10.0	3	6	CF306759	HDAL--04-
C 854	1	10.0	2	7	CK632229	CK632229	AML--AM000	927	1	10.0	3	6	CF306836	HDAL--04-
C 855	1	10.0	2	7	CK632229	CK632229	AML--AM000	C 928	1	10.0	3	6	CF306836	HDAL--04-
C 856	1	10.0	2	7	CK632229	CK632229	AML--AM000	929	1	10.0	3	6	CF306855	HDAL--05-
C 857	1	10.0	2	8	BH754642	BH754642	SALK_0430	C 930	1	10.0	3	6	CF306855	HDAL--05-
C 858	1	10.0	2	8	BH754642	BH754642	SALK_0430	931	1	10.0	3	6	CF306855	HDAL--05-
C 859	1	10.0	2	8	BH754642	BH754642	SALK_0430	C 932	1	10.0	3	6	CF306874	HDAL--05-
C 860	1	10.0	2	8	BH754642	BH754642	SALK_0430	933	1	10.0	3	6	CF306874	HDAL--05-
C 861	1	10.0	2	8	BH754642	BH754642	SALK_0430	C 934	1	10.0	3	6	CF306921	HDAL--05-
C 862	1	10.0	2	9	CL423384	CL423384	01S0554-0	935	1	10.0	3	6	CF306921	HDAL--05-
C 863	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 936	1	10.0	3	6	CF306992	HDAL--05-
C 864	1	10.0	2	9	CL423384	CL423384	01S0554-0	937	1	10.0	3	6	CF306992	HDAL--05-
C 865	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 938	1	10.0	3	6	CF307052	HDAL--05-
C 866	1	10.0	2	9	CL423384	CL423384	01S0554-0	939	1	10.0	3	6	CF307052	HDAL--05-
C 867	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 940	1	10.0	3	6	CF307058	HDAL--05-
C 868	1	10.0	2	9	CL423384	CL423384	01S0554-0	941	1	10.0	3	6	CF307058	HDAL--05-
C 869	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 942	1	10.0	3	6	CF307069	HDAL--05-
C 870	1	10.0	2	9	CL423384	CL423384	01S0554-0	943	1	10.0	3	6	CF307069	HDAL--05-
C 871	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 944	1	10.0	3	6	CF307073	HDAL--05-
C 872	1	10.0	2	9	CL423384	CL423384	01S0554-0	945	1	10.0	3	6	CF307073	HDAL--05-
C 873	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 946	1	10.0	3	6	CF307112	HDAL--05-
C 874	1	10.0	2	9	CL423384	CL423384	01S0554-0	947	1	10.0	3	6	CF307112	HDAL--05-
C 875	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 948	1	10.0	3	6	CF307117	HDAL--05-
C 876	1	10.0	2	9	CL423384	CL423384	01S0554-0	949	1	10.0	3	6	CF307117	HDAL--05-
C 877	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 950	1	10.0	3	6	CF307203	HDAL--06-
C 878	1	10.0	2	9	CL423384	CL423384	01S0554-0	951	1	10.0	3	6	CF307203	HDAL--06-
C 879	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 952	1	10.0	3	6	CF307223	HDAL--06-
C 880	1	10.0	2	9	CL423384	CL423384	01S0554-0	953	1	10.0	3	6	CF307223	HDAL--06-
C 881	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 954	1	10.0	3	6	CF307246	HDAL--06-
C 882	1	10.0	2	9	CL423384	CL423384	01S0554-0	955	1	10.0	3	6	CF307246	HDAL--06-
C 883	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 956	1	10.0	3	6	CF307290	HDAL--06-
C 884	1	10.0	2	9	CL423384	CL423384	01S0554-0	957	1	10.0	3	6	CF307290	HDAL--06-
C 885	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 958	1	10.0	3	6	CF307313	HDAL--06-
C 886	1	10.0	2	9	CL423384	CL423384	01S0554-0	959	1	10.0	3	6	CF307313	HDAL--06-
C 887	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 960	1	10.0	3	6	CF307367	HDAL--06-
C 888	1	10.0	2	9	CL423384	CL423384	01S0554-0	961	1	10.0	3	6	CF307367	HDAL--06-
C 889	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 962	1	10.0	3	6	CF307404	HDAL--06-
C 890	1	10.0	2	9	CL423384	CL423384	01S0554-0	963	1	10.0	3	6	CF307404	HDAL--06-
C 891	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 964	1	10.0	3	6	CF307480	HDAL--06-
C 892	1	10.0	2	9	CL423384	CL423384	01S0554-0	965	1	10.0	3	6	CF307480	HDAL--06-
C 893	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 966	1	10.0	3	6	CF307489	HDAL--06-
C 894	1	10.0	2	9	CL423384	CL423384	01S0554-0	967	1	10.0	3	6	CF307489	HDAL--06-
C 895	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 968	1	10.0	3	6	CF307511	HDAL--06-
C 896	1	10.0	2	9	CL423384	CL423384	01S0554-0	969	1	10.0	3	6	CF307511	HDAL--06-
C 897	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 970	1	10.0	3	6	CF307516	HDAL--06-
C 898	1	10.0	2	9	CL423384	CL423384	01S0554-0	971	1	10.0	3	6	CF307516	HDAL--06-
C 899	1	10.0	2	9	CL423384	CL423384	01S0554-0	C 972	1	10.0	3	6	CF307535	HDAL--06-
C 900	1	10.0	2	9	CL423384	CL423384	01S0554-0	973	1	10.0	3	6	CF307535	HDAL--06-

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c 974      1 10.0      3 6 CF308858
c 975      1 10.0      3 6 CF309377
c 976      1 10.0      3 6 CF309377
c 977      1 10.0      3 6 CF310006
c 978      1 10.0      3 6 CF310006
c 979      1 10.0      3 6 CF310006
c 980      1 10.0      3 6 CF311041
c 981      1 10.0      3 6 CF311041
c 982      1 10.0      3 6 CF311214
c 983      1 10.0      3 6 CF311214
c 984      1 10.0      3 6 CF311628
c 985      1 10.0      3 6 CF311628
c 986      1 10.0      3 6 CF313258
c 987      1 10.0      3 6 CF313258
c 988      1 10.0      3 6 CF315089
c 989      1 10.0      3 6 CF315089
c 990      1 10.0      3 6 CF315183
c 991      1 10.0      3 6 CF315183
c 992      1 10.0      3 6 CF315632
c 993      1 10.0      3 6 CF315632
c 994      1 10.0      3 6 CF317717
c 995      1 10.0      3 6 CF317717
c 996      1 10.0      3 6 CF322001
c 997      1 10.0      3 6 CF322001
c 998      1 10.0      3 6 CF327094
c 999      1 10.0      3 6 CF327094
c1000     1 10.0      3 6 CF334168
c1000     1 10.0      3 6 CF334168

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## ALIGNMENTS

```

RESULT 1
CNS015BQ      74 bp      DNA      linear      GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION      BACN13P24 of DrosBAC library from Drosophila melanogaster (fruit
ACCESSION      AL105248
VERSION      AL105248.1 GI:5617262
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 74)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT      - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES      Location/Qualifiers
source      1..74
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            /mol_type="genomic DNA"
            /db_xref="taxon:7227"
            /clone="BACN13P24"
            /clone_lib="DrosBAC"
            /plasmid="pBelobAC11"
            /note="end : SP6"

ORIGIN
Query Match      40.0%; Score 4; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWWG 7
Db      71 CWWG 68

RESULT 3
AF211608      77 bp      mRNA      linear      EST 31-DEC-2000
LOCUS      AF211608 34.1B Nicotiana tabacum cDNA clone fragment 79, mRNA
DEFINITION      sequence.
ACCESSION      AF211608
VERSION      AF211608.1 GI:11999989
KEYWORDS      EST.
SOURCE      Nicotiana tabacum (common tobacco)
ORGANISM      Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE      1 (bases 1 to 77)
AUTHORS      Durrant,W.E., Rowland,O., Piedras,P., Hammond-Kosack,K.E. and
Jones,J.D.G.
TITLE      cDNA expression profiling reveals rapid, resistance gene-dependent,
active oxygen-independent, gene induction during the plant defence

```

response  
Unpublished (1999)  
Contact: Durrant WE  
Sainsbury Laboratory  
John Innes Centre  
Colney Lane, Norwich, Norfolk NR4 7UH, UK  
Email: wendy.durrant@bbsrc.ac.uk  
rapidly induced, oxidative burst independent cDNA-AFLP fragment.

FEATURES  
source  
1..77  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/cultivar="Petite Havana"  
/db\_xref="taxon:4097"  
/clone="fragment 79"  
/clone\_lib="34.1B"  
/note="cell suspension cultures harvested 30 min after treatment with the Avr9 peptide from the fungus Cladosporium fulvum; 34.1B tobacco contains Cf-9 resistance gene"

ORIGIN  
Query Match 40.0%; Score 4; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RCW 5  
|||||  
Db 30 RCW 33

RESULT 4  
AF211608/c  
LOCUS AF211608 77 bp mRNA linear EST 31-DEC-2000  
DEFINITION AF211608 34.1B Nicotiana tabacum cDNA clone fragment 79, mRNA sequence.  
ACCESSION AF211608  
VERSION AF211608.1 GI:11999989  
KEYWORDS EST.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 77)  
AUTHORS Durrant, W.E., Rowland, O., Piedras, P., Hammond-Kosack, K.E. and Jones, J.D.G.  
TITLE cDNA expression profiling reveals rapid, resistance gene-dependent, active oxygen-independent, gene induction during the plant defence response  
JOURNAL Unpublished (1999)  
COMMENT Contact: Durrant WE  
Sainsbury Laboratory  
John Innes Centre  
Colney Lane, Norwich, Norfolk NR4 7UH, UK  
Email: wendy.durrant@bbsrc.ac.uk  
rapidly induced, oxidative burst independent cDNA-AFLP fragment.

FEATURES  
source  
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/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/cultivar="Petite Havana"  
/db\_xref="taxon:4097"  
/clone="fragment 79"  
/clone\_lib="34.1B"  
/note="cell suspension cultures harvested 30 min after treatment with the Avr9 peptide from the fungus Cladosporium fulvum; 34.1B tobacco contains Cf-9 resistance gene"

ORIGIN  
Query Match 40.0%; Score 4; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 WGY 9  
|||||  
Db 33 WGY 30

RESULT 5  
AY431131  
LOCUS AY431131 63 bp mRNA linear HTC 23-JUN-2004  
DEFINITION Aedes aegypti ASAP ID: 38277 unknown mRNA sequence.  
ACCESSION AY431131  
VERSION AY431131.1 GI:42762112  
KEYWORDS HTC.  
SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.  
TITLE Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subbalatus  
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)  
PUBMED 15213157  
REFERENCE 2 (bases 1 to 63)  
AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.  
TITLE Direct Submission  
JOURNAL Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA  
COMMENT More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ahabs.wisc.edu/annotation/php/logon.php>.  
FEATURES  
source  
1..63  
/organism="Aedes aegypti"  
/mol\_type="mRNA"  
/strain="liverpool"  
/isolation\_source="perfused hemolymph of bacteria-inoculated organisms at 1, 3, 6, 12, and 24 hours post-inoculation"  
/db\_xref="taxon:7159"  
/sex="female"  
/cell\_type="hemocyte"  
/tissue\_type="hemolymph"  
/dev\_stage="adult"  
/note="ASAP-UW Feature ID: 38276"  
misc\_feature 1..63  
/note="unknown; ASAP-UW Feature ID: 38277"

ORIGIN  
Query Match 30.0%; Score 3; DB 3; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCW 5  
|||||  
Db 30 RCW 32

RESULT 6  
AY431131/c  
LOCUS AY431131 63 bp mRNA linear HTC 23-JUN-2004

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DEFINITION Aedes aegypti ASAP ID: 38277 unknown mRNA sequence.
ACCESSION AY431131
VERSION AY431131.1 GI:42762112
KEYWORDS HTC.
SOURCE Aedes aegypti
ORGANISM Aedes aegypti (yellow fever mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.
REFERENCE 1 (bases 1 to 63)
AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
Fuchs, J.F., Russ, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
Christensen, B.M.
TITLE Description of the Transcriptomes of Immune Response-Activated
Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
subalbatus
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED 15213157
REFERENCE 2 (bases 1 to 63)
AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
Liss, P., Russ, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K.,
Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C.,
Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
53706, USA
COMMENT More information about this sequence is available in ASAP (A
Systematic Annotation Package for community analysis of genomes)
from the University of Wisconsin-Madison at
https://asap.ababa.wisc.edu/annotation/php/logon.php.
FEATURES
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        Location/Qualifiers
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                /mol_type="mRNA"
                /strain="liverpool"
                /isolation_source="perfused hemolymph of
bacteria-inoculated organisms at 1, 3, 6, 12, and 24
hours post-inoculation"
                /db_xref="taxon:7159"
                /sex="female"
                /cell_type="hemocyte"
                /tissue_type="hemolymph"
                /dev_stage="adult"
                /note="ASAP-UW Feature ID: 38276"
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                1..63
                    /note="unknown; ASAP-UW Feature ID: 38277"
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            Best Local Similarity 100.0%; Pred. No. 0;
            Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGY 8
DB 32 WGY 30

RESULT 7
CONS011MQ 68 bp DNA linear GSS 26-JUL-1999
LOCUS BACN06B15 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
DEFINITION fly), genomic survey sequence.
ACCESSION AL100460
VERSION AL100460.1 GI:5612071
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephyrdoidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 68)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
    source
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            1..68
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                /clone="BACN06B15"
                /clone_lib="DrosBAC"
                /plasmid="pBelobAC11"
                /note="end : T7"
        ORIGIN
            Query Match 30.0%; Score 3; DB 9; Length 68;
            Best Local Similarity 100.0%; Pred. No. 0;
            Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 6
DB 1 CW 3

RESULT 8
CONS011MQ/c 68 bp DNA linear GSS 26-JUL-1999
LOCUS BACN06B15 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
DEFINITION fly), genomic survey sequence.
ACCESSION AL100460
VERSION AL100460.1 GI:5612071
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephyrdoidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 68)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
    source
        Location/Qualifiers
            1..68
                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /db_xref="taxon:7227"
                /clone="BACN06B15"
                /clone_lib="DrosBAC"
                /plasmid="pBelobAC11"
                /note="end : T7"
        ORIGIN

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Query Match 30.0%; Score 3; DB 9; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WVG 7  
 ||||  
 Db 3 WVG 1

RESULT 9  
 T24836  
 LOCUS EST411 Human colorectal cancer Homo sapiens cDNA clone 15C4, mRNA  
 DEFINITION

ACCESSION T24836  
 VERSION T24836.1 GI:534461  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 70)  
 AUTHORS Frigerio,J.-M., Berthezene,P., Garrido,P., Ortiz,E., Barthelmy,S,  
 Vasseur,S., Sastre,B., Seleznieff,I., Dagorn,J.-C. and  
 Iovanna,J.-L.

TITLE Analysis of 2166 clones from a human colorectal cancer cDNA library  
 by partial sequencing

JOURNAL Hum. Mol. Genet. 4, 37-43 (1995)  
 MEDLINE 95227175  
 PUBMED 7711732

COMMENT Contact: Iovanna JL  
 U.315 INSERM  
 46 Bd de la Gaye, F-13009 Marseille, France.  
 Tel: (33) 91 82 03 15  
 Fax: (33) 91 26 62 19

Email: dagorn@arthur.cit12.fr  
 This sequence is one of a series obtained by systematic sequencing  
 of a colorectal cancer cDNA library.  
 Seq primer: M13 Forward.

FEATURES  
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 1..70  
 /organism="Homo sapiens"  
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 /clone\_lib="Human colorectal cancer"  
 /note="Vector: pT7T3D; Site 1: Eco RI; Site 2: Not I; mRNA  
 was purified from a colorectal tumour of an adult male.  
 cDNA was constructed and cloned into the pT7T3D phagemid  
 following the manufacturer instructions (Pharmacia)."

## ORIGIN

Query Match 30.0%; Score 3; DB 7; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWV 6  
 ||||  
 Db 17 CWV 19

RESULT 10  
 T24836/c  
 LOCUS EST411 Human colorectal cancer Homo sapiens cDNA clone 15C4, mRNA  
 DEFINITION

ACCESSION T24836  
 VERSION T24836.1 GI:534461  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE  
AUTHORSTITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Iovanna JL  
 U.315 INSERM  
 46 Bd de la Gaye, F-13009 Marseille, France.  
 Tel: (33) 91 82 03 15  
 Fax: (33) 91 26 62 19  
 Email: dagorn@arthur.cit12.fr  
 This sequence is one of a series obtained by systematic sequencing  
 of a colorectal cancer cDNA library.  
 Seq primer: M13 Forward.

FEATURES  
source

1..70  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="15C4"  
 /lab\_host="E. coli NM522"  
 /clone\_lib="Human colorectal cancer"  
 /note="Vector: pT7T3D; Site 1: Eco RI; Site 2: Not I; mRNA  
 was purified from a colorectal tumour of an adult male.  
 cDNA was constructed and cloned into the pT7T3D phagemid  
 following the manufacturer instructions (Pharmacia)."

## ORIGIN

Query Match 30.0%; Score 3; DB 7; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WVG 7  
 ||||  
 Db 19 WVG 17

RESULT 11  
LOCUS

DEFINITION 4A3A-P8D3-R Anopheles gambiae immune competent 4A3A Anopheles  
 gambiae cDNA clone 4A3A-P8D3, mRNA sequence.

ACCESSION AJ283222  
 VERSION AJ283222.1 GI:6931101  
 KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Anopheles.

1 (bases 1 to 88)

Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,  
 Donohue,M., Schultz,J., Benes,V., Bork,P., Ansoorge,W., Soares,M.B.  
 and Kafatos,F.C.

Anopheles gambiae pilot gene discovery project: identification of  
 mosquito innate immunity genes from expressed sequence tags  
 generated from immune-competent cell lines  
 Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL 20300950  
 MEDLINE 10841561  
 PUBMED

COMMENT Contact: Dimopoulos G  
 Fotis C. Kafatos laboratory  
 European Molecular Biology Laboratory  
 Meyerhofstrasse 1, 69117 Heidelberg, Germany.

FEATURES  
source

1..88  
 /organism="Anopheles gambiae"

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/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
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/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."

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## ORIGIN

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Query Match      30.0%; Score 3; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 WWG 7
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Db      39 WWG 41

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RESULT 12
AJ283222/c
LOCUS      88 bp mRNA linear EST 30-JUN-2000
DEFINITION 4A3A-P8D3-R Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P8D3, mRNA sequence.
ACCESSION  AJ283222
VERSION     AJ283222.1 GI:69311101
KEYWORDS   EST.
SOURCE     Anopheles gambiae (African malaria mosquito)
ORGANISM   Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
Anopheles.

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REFERENCE  1 (bases 1 to 88)
AUTHORS   Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.
TITLE     mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE   20300950
PUBMED    10841561
COMMENT   Contact: Dimopoulos G
          Fotis C. Kafatos laboratory
          European Molecular Biology Laboratory
          Meyerhofstrasse 1, 69117 Heidelberg, Germany.

```

```

FEATURES
source
Location/Qualifiers
1..88
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P8D3"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."

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## ORIGIN

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Query Match      30.0%; Score 3; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 CWW 6
      |||
Db      41 CWW 39

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RESULT 13
T24971
LOCUS      90 bp mRNA linear EST 24-AUG-1995
DEFINITION EST546 Human colorectal cancer Homo sapiens cDNA clone 19E1, mRNA
sequence.
ACCESSION  T24971
VERSION     T24971.1 GI:534596
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE  1 (bases 1 to 90)
AUTHORS   Frigerio, J.-M., Berthezene, P., Garrido, P., Ortiz, E., Barthelmy, S.,
Vasseur, S., Sastre, B., Seleznieff, I., Dagorn, J.-C. and
Iovanna, J.-L.
TITLE     Analysis of 2166 clones from a human colorectal cancer cDNA library
by partial sequencing
JOURNAL   Hum. Mol. Genet. 4, 37-43 (1995)
MEDLINE   95227175
PUBMED    7711732
COMMENT   Contact: Iovanna JL
          U.315 INSERM
          46 Bd de la Gaye, F-13009 Marseille, France.
          Tel: (33) 91 82 03 15
          Fax: (33) 91 26 62 19
          Email: dagorn@arthur.citil2.fr
          This sequence is one of a series obtained by systematic sequencing
          of a colorectal cancer cDNA library.
          Seq primer: M13 Forward.

```

```

FEATURES
source
Location/Qualifiers
1..90
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="19E1"
/lab_host="E. coli NM522"
/clone_lib="Human colorectal cancer"
/notes="Vector: pT7T3D; Site 1: Eco RI; Site 2: Not I; mRNA
was purified from a colorectal tumour of an adult male.
cDNA was constructed and cloned into the pT7T3D phagemid
following the manufacturer instructions (Pharmacia)."

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## FEATURES

source

Location/Qualifiers

1..90

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="19E1"

/lab\_host="E. coli NM522"

/clone\_lib="Human colorectal cancer"

/notes="Vector: pT7T3D; Site 1: Eco RI; Site 2: Not I; mRNA

was purified from a colorectal tumour of an adult male.

cDNA was constructed and cloned into the pT7T3D phagemid

following the manufacturer instructions (Pharmacia)."

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 90)  
Frigerio, J.-M., Berthezene, P., Garrido, P., Ortiz, E., Barthelémy, S.,  
Vasseur, S., Sastre, B., Seleznieff, I., Dagorn, J.-C. and  
Iovanna, J.-L.  
Analysis of 2166 clones from a human colorectal cancer cDNA library  
by partial sequencing  
Hum. Mol. Genet. 4, 37-43 (1995)  
9527175  
7711732  
Contact: Iovanna JL  
U.315 INSERM  
46 Bd de la Gaye, F-13009 Marseille, France.  
Tel: (33) 91 82 03 15  
Fax: (33) 91 26 62 19  
Email: dagorn@arthur.cit12.fr

This sequence is one of a series obtained by systematic sequencing  
of a colorectal cancer cDNA library.  
Seq primer: M13 Forward.

FEATURES  
source

Location/Qualifiers  
1..90  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="19E1"  
/lab\_host="E. coli NM522"  
/clone\_lib="Human colorectal cancer"  
/note="Vector: pT73D; Site\_1: Eco RI; Site\_2: Not I; mRNA  
was purified from a colorectal tumour of an adult male.  
cDNA was constructed and cloned into the pT73D phagemid  
following the manufacturer instructions (Pharmacia)."

ORIGIN

Query Match 30.0%; Score 3; DB 7; Length 90;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
|||  
Db 29 GY 27

RESULT 15  
BQ704626  
LOCUS  
DEFINITION  
Bn01\_03123 A 91 bp mRNA linear EST 16-JUL-2002  
Bn01\_AAPC\_ECORC\_transgenic\_Brassica\_napus\_overexpressing\_BNCBF17.co  
nstitutively\_frost\_tolerant Brassica napus cDNA clone Bn01\_03123,  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ704626  
BQ704626.1 GI:21844045  
EST.  
Brassica napus (rape)  
Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 91)  
Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,  
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.  
Expressed Sequence Tags from constitutively frost tolerant  
transgenic Brassica napus overexpressing BNCBF17  
Unpublished (2002)  
Contact: Singh, J.A.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA  
OC6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@agr.gc.ca.

FEATURES  
source

Location/Qualifiers  
1..91

/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Westar"  
/db\_xref="taxon:3708"  
/clone="Bn01\_03123"  
/tissue\_type="fourth leaf"

/dev\_stage="3 weeks seedling grown at room temperature"  
/clone\_lib="Bn01\_AAPC\_ECORC\_transgenic\_Brassica\_napus\_over  
expressing\_BNCBF17\_constitutively\_frost\_tolerant"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;  
Site 2: XhoI; Germinated in soil flats and seedlings grown  
for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr  
light (250 Em-2sec-1) and 16°C / 8 hr dark. Fourth leaves  
collected at 9 am and immediately frozen."

ORIGIN

Query Match 30.0%; Score 3; DB 5; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 35 RRC 37

RESULT 16  
BQ704626/c  
LOCUS  
DEFINITION

BQ704626 91 bp mRNA linear EST 16-JUL-2002  
Bn01\_03123 A  
Bn01\_AAPC\_ECORC\_transgenic\_Brassica\_napus\_overexpressing\_BNCBF17.co  
nstitutively\_frost\_tolerant Brassica napus cDNA clone Bn01\_03123,  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ704626  
BQ704626.1 GI:21844045  
EST.  
Brassica napus (rape)  
Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 91)  
Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,  
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.  
Expressed Sequence Tags from constitutively frost tolerant  
transgenic Brassica napus overexpressing BNCBF17  
Unpublished (2002)  
Contact: Singh, J.A.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA  
OC6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@agr.gc.ca.

FEATURES  
source

Location/Qualifiers  
1..91  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Westar"  
/db\_xref="taxon:3708"  
/clone="Bn01\_03123"  
/tissue\_type="fourth leaf"

/dev\_stage="3 weeks seedling grown at room temperature"  
/clone\_lib="Bn01\_AAPC\_ECORC\_transgenic\_Brassica\_napus\_over  
expressing\_BNCBF17\_constitutively\_frost\_tolerant"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;  
Site 2: XhoI; Germinated in soil flats and seedlings grown  
for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr  
light (250 Em-2sec-1) and 16°C / 8 hr dark. Fourth leaves  
collected at 9 am and immediately frozen."

ORIGIN

Query Match 30.0%; Score 3; DB 5; Length 91;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9
   |||
Db 37 GY 35

RESULT 17
AY431374
LOCUS AY431374 92 bp mRNA linear HTC 24-JUN-2004
DEFINITION Aedes aegypti ASAP ID: 36897 unknown mRNA sequence.
ACCESSION AY431374
VERSION AY431374.1 GI:42763516
KEYWORDS HTC.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
          Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
          Stegomyia.
REFERENCE 1 (bases 1 to 92)
AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
          Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
          Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
          Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
          Christensen,B.M.
TITLE Description of the Transcriptomes of Immune Response-Activated
          Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
          subalbatus
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED 15213157
REFERENCE 2 (bases 1 to 92)
AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
          Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
          Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
          Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
          University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
          53706, USA
COMMENT More information about this sequence is available in ASAP (A
          Systematic Annotation Package for community analysis of genomes)
          from the University of Wisconsin-Madison at
          https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES
          source
          1..92
          /organism="Aedes aegypti"
          /mol_type="mRNA"
          /strain="liverpool"
          /isolation_source="perfused hemolymph of
          bacteria-inoculated organisms at 1, 3, 6, 12, and 24
          hours post-inoculation"
          /db_xref="taxon:7159"
          /sex="female"
          /cell_type="hemocyte"
          /tissue_type="hemolymph"
          /dev_stage="adult"
          /note="ASAP-UW Feature ID: 36896"
          misc_feature 1..92
          /note="unknown; ASAP-UW Feature ID: 36897"
          ORIGIN
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          Best Local Similarity 100.0%; Pred. No. 0;
          Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
   |||
Db 9 WWG 7

RESULT 19
CNS00Y20
LOCUS CNS00Y20 93 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
          BACN01A02 of DrosBAC library from Drosophila melanogaster (fruit
          fly), genomic survey sequence.
ACCESSION AL097014
VERSION AL097014.1 GI:5608625
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Query Match 30.0%; Score 3; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 6
   |||
Db 7 CW 9

RESULT 18
AY431374/c

```



Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 93)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

#### FEATURES

source

Location/Qualifiers  
1. .93  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN01A02"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : SP6"

#### ORIGIN

Query Match 30.0%; Score 3; DB 9; Length 93;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10

Db 70 YY 72

RESULT 20

CNS00YZ0/c

LOCUS

DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACN01A02 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 93)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

#### FEATURES

source

Location/Qualifiers  
1. .93  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN01A02"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : SP6"

#### ORIGIN

Query Match 30.0%; Score 3; DB 9; Length 93;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3

Db 72 RRR 70

RESULT 21

CNS01070

LOCUS

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN03G10 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 96)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

#### FEATURES

source

Location/Qualifiers  
1. .96  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN03G10"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

Query Match 30.0%; Score 3; DB 9; Length 96;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7

Db 2 WWG 4

RESULT 22

CNS01070/c

LOCUS

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN03G10 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

```

REFERENCE
AUTHORS      1 (bases 1 to 96)
TITLE        Genoscope.
JOURNAL      Direct Submission
             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
             collaboration with the European Drosophila Genome Project (EDGP) -
             http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
             library (Dros BAC) was made by Alain Billault at CEPH (Centre
             d'Etude du Polymorphisme Humain) with funding provided by a MRC
             project grant. The DNA was prepared from embryos by Alain Bucheton
             and Genevieve Payan. It has been constructed in the vector
             pBelobAC11.
FEATURES     Location/Qualifiers
             source          1..96
                             /organism="Drosophila melanogaster"
                             /mol_type="genomic DNA"
                             /db_xref="taxon:7227"
                             /clone="BACN03G10"
                             /clone_lib="DrosBAC"
                             /plasmid="pBelobAC11"
                             /note="end : T7"
ORIGIN
Query Match      30.0%; Score 3; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
        |||
        4 CWW 2

RESULT 23
CNS0429N
LOCUS      CNS0429N          98 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            075N24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL271220
VERSION     AL271220.1 GI:7993184
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL     20296633
MEDLINE     PUBMED
REFERENCE   2
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
JOURNAL     20359837
MEDLINE     PUBMED
REFERENCE   3 (bases 1 to 98)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT      This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES     Location/Qualifiers
             source          1..98
                             /organism="Tetraodon nigroviridis"
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                             /db_xref="taxon:99883"
                             /clone="075N24"
                             /clone_lib="G"
             /note="Genoscope sequence ID : COBG075DG12LP1-end : T7"

```



Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

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1. .30
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR25K03"
/clone_lib="RPCT-98"
/note="end : TET3"
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## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5  
||  
Db 26 CW 27

RESULT 28  
CNS00C45/c

## LOCUS

## DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR25K03 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## ACCESSION

AL058402

## VERSION

AL058402.1

## KEYWORDS

GSS.

## SOURCE

Drosophila melanogaster (fruit fly)

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 30)

## REFERENCE

Genoscope.

Direct Submission

Submitted (02-JUN-1999)

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCT-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

1. .30

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

/clone="BACR25K03"

/clone\_lib="RPCT-98"

/note="end : TET3"

## ORIGIN

## Query Match

Best Local Similarity

Matches

2; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

6 WG 7

||

Db

27 WG 26

||

RESULT 29

CNS00JBW

## LOCUS

## DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR38L23 of RPCT-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL075982

AL075982.1

GI:4955661

GSS.

## SOURCE

Drosophila melanogaster (fruit fly)

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 36)

## REFERENCE

Genoscope.

Direct Submission

Submitted (02-JUN-1999)

Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCT-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

1. .36

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

/clone="BACR38L23"

/clone\_lib="RPCT-98"

/note="end : T7"

## ORIGIN

Query Match

Best Local Similarity

Matches

2; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

3 RC 4

||

Db

27 RC 28

||

RESULT 30

CNS00JBW/c

## LOCUS

## DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR38L23 of RPCT-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL075982

AL075982.1

GI:4955661

GSS.

## SOURCE

Drosophila melanogaster (fruit fly)

```

ORGANISM      Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 36)
AUTHORS       Genoscope.
TITLE         Direct Submission
JOURNAL       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
               BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
               - Web : www.genoscope.cns.fr)
COMMENT       Determination of this BAC-end sequence was carried out as part of a
               collaboration with the Berkeley Drosophila Genome Project (BDGP).
               The BDGP is constructing a physical map of the Drosophila
               melanogaster genome using these BACs. For further information
               please see http://www.fruitfly.org The BDGP Drosophila
               melanogaster BAC library was prepared by Kazutoyo Osoegawa and
               Aaron Mammosser in Pieter de Jong's laboratory in the Department of
               Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
               NY. The library is named RPCI-98 and was constructed by partial
               EcoRI digestion of Drosophila DNA provided by the BDGP from the
               isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
               p1 and EST libraries. A more detailed description of the library
               and how to order individual BAC clones, the entire library, or
               filters for hybridization from the BACPAC Resource Center can be
               found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES      source
               1..36
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR38L23"
               /clone_lib="RPCI-98"
               /note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8
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Db 28 GY 27

RESULT 31
CNS00L8C
LOCUS      CNS00L8C              38 bp      DNA      linear      GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR24P20 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL068197
VERSION     AL068197.1 GI:4958134
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammosser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES      source
               1..38
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR24P20"
               /clone_lib="RPCI-98"
               /note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
   ||
Db 22 RC 23

RESULT 32
CNS00L8C/c
LOCUS      CNS00L8C/c          38 bp      DNA      linear      GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR24P20 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL068197
VERSION     AL068197.1 GI:4958134
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammosser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES      source
               1..38
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR24P20"
               /clone_lib="RPCI-98"
               /note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES      source
               1..38
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR24P20"
               /clone_lib="RPCI-98"
               /note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
   ||
Db 22 RC 23

RESULT 32
CNS00L8C
LOCUS      CNS00L8C              38 bp      DNA      linear      GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR24P20 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL068197
VERSION     AL068197.1 GI:4958134
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
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            Aaron Mammosser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES      source
               1..38
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR24P20"
               /clone_lib="RPCI-98"
               /note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      7 GY 8
Db      27 GY 26

RESULT 33
AW059591 LOCUS
DEFINITION HUTH.bsst.dnc15.final.cluster_81_(3) DNC15 Homo sapiens cDNA
similar to LD78, mRNA sequence.
ACCESSION AW059591
VERSION   AW059591.1 GI:6651913
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
          McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,
          Burcham,T. and Albrecht,G.
          In vitro cloning of complex mixtures of DNA on microbeads: Physical
          separation of differentially expressed cDNAs
          Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
          20144098
          10677516
COMMENT   Contact: Burcham TS
          LYNX Therapeutics, Inc.
          25861 Industrial Blvd., Hayward, CA 94545, USA
          Tel: 510 670 9338
          Fax: 510 670 9302
          Email: timb@lynxgen.com
          Sequence obtained from LYNX Therapeutics Megasort technology.
          Collected from the down-regulated gate. Consensus sequence of 3
          sequences in cluster.
          High quality sequence stop: 41.
          Location/Qualifiers
            1..41
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /cell_type="monocytic leukemia"
              /cell_line="THP-1 (TIB-202)"
              /clone_lib="DNC15"
              /note="Vector: pCR2.1; Cloning of PCR products from
              micro-beads carrying 3' end of down-regulated cDNA. THP-1
              cells non-induced (treated with DMSO only)."

ORIGIN
Query Match      20.0%; Score 2; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 8
Db      15 GY 14

RESULT 35
AW059842 LOCUS
DEFINITION HUTH.bsst.upc15.final.cluster_1(363) UPC15 Homo sapiens cDNA
similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.
ACCESSION AW059842
VERSION   AW059842.1 GI:6652164
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
          McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,
          Burcham,T. and Albrecht,G.
          In vitro cloning of complex mixtures of DNA on microbeads: Physical
          separation of differentially expressed cDNAs
          Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
          20144098
          10677516
COMMENT   Contact: Burcham TS
          LYNX Therapeutics, Inc.
          25861 Industrial Blvd., Hayward, CA 94545, USA
          Tel: 510 670 9338
          Fax: 510 670 9302
          Email: timb@lynxgen.com
          Sequence obtained from LYNX Therapeutics Megasort technology.
          Collected from the up-regulated gate. Consensus sequence of 363
          sequences in cluster.
          High quality sequence stop: 41.
          Location/Qualifiers
            1..41
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FEATURES
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  /cell_line="THP-1 (TIB-202)"
  /clone_lib="DNC15"
  /note="Vector: pCR2.1; Cloning of PCR products from
  micro-beads carrying 3' end of down-regulated cDNA. THP-1
  cells non-induced (treated with DMSO only)."

ORIGIN
Query Match      20.0%; Score 2; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RC 4
Db      14 RC 15

RESULT 34
AW059591/c LOCUS
DEFINITION HUTH.bsst.dnc15.final.cluster_81_(3) DNC15 Homo sapiens cDNA
similar to LD78, mRNA sequence.
ACCESSION AW059591
VERSION   AW059591.1 GI:6651913
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
          McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,
          Burcham,T. and Albrecht,G.
          In vitro cloning of complex mixtures of DNA on microbeads: Physical
          separation of differentially expressed cDNAs
          Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
          20144098
          10677516
COMMENT   Contact: Burcham TS
          LYNX Therapeutics, Inc.
          25861 Industrial Blvd., Hayward, CA 94545, USA
          Tel: 510 670 9338
          Fax: 510 670 9302
          Email: timb@lynxgen.com
          Sequence obtained from LYNX Therapeutics Megasort technology.
          Collected from the down-regulated gate. Consensus sequence of 3
          sequences in cluster.
          High quality sequence stop: 41.
          Location/Qualifiers
            1..41
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /cell_type="monocytic leukemia"
              /cell_line="THP-1 (TIB-202)"
              /clone_lib="DNC15"
              /note="Vector: pCR2.1; Cloning of PCR products from
              micro-beads carrying 3' end of down-regulated cDNA. THP-1
              cells non-induced (treated with DMSO only)."

ORIGIN
Query Match      20.0%; Score 2; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RC 4
Db      14 RC 15

RESULT 34
AW059591/c LOCUS
DEFINITION HUTH.bsst.dnc15.final.cluster_81_(3) DNC15 Homo sapiens cDNA
similar to LD78, mRNA sequence.
ACCESSION AW059591
VERSION   AW059591.1 GI:6651913
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
          McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,
          Burcham,T. and Albrecht,G.
          In vitro cloning of complex mixtures of DNA on microbeads: Physical
          separation of differentially expressed cDNAs
          Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
          20144098
          10677516
COMMENT   Contact: Burcham TS
          LYNX Therapeutics, Inc.
          25861 Industrial Blvd., Hayward, CA 94545, USA
          Tel: 510 670 9338
          Fax: 510 670 9302
          Email: timb@lynxgen.com
          Sequence obtained from LYNX Therapeutics Megasort technology.
          Collected from the up-regulated gate. Consensus sequence of 363
          sequences in cluster.
          High quality sequence stop: 41.
          Location/Qualifiers
            1..41
              /organism="Homo sapiens"

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TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,  
Burcham,T. and Albrecht,G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
20144098  
10677516

Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com

Sequence obtained from LYNX Therapeutics Megasort technology.  
Collected from the down-regulated gate. Consensus sequence of 3  
sequences in cluster.  
High quality sequence stop: 41.

FEATURES  
source  
1..41  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"  
/note="Vector: pCR2.1; Cloning of PCR products from  
micro-beads carrying 3' end of down-regulated cDNA. THP-1  
cells non-induced (treated with DMSO only)."

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
Db 15 GY 14

RESULT 35

AW059842 LOCUS  
DEFINITION HUTH.bsst.upc15.final.cluster\_1(363) UPC15 Homo sapiens cDNA  
similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.  
ACCESSION AW059842  
VERSION AW059842.1 GI:6652164  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 41)

Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,  
McCollum,C., Mao,J.I., Kirchmer,J.J., Eletr,S., DuBridge,R.B.,  
Burcham,T. and Albrecht,G.

In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
20144098  
10677516

COMMENT

Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com

Sequence obtained from LYNX Therapeutics Megasort technology.  
Collected from the up-regulated gate. Consensus sequence of 363  
sequences in cluster.  
High quality sequence stop: 41.

FEATURES  
source  
1..41  
Location/Qualifiers  
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="UPC15"
/notes="Vector: pCR2.1; Cloning of PCR products from
micro-beads carrying 3' end of up-regulated cDNA. THP-1
cells induced with 100 nM PMA in DMSO. "
```

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
||  
Db 27 GY 28

RESULT 36  
AW059842/c  
LOCUS  
DEFINITION HuTh.best.upc15.final.cluster\_1(363) UPC15 Homo sapiens cDNA  
similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.

ACCESSION AW059842  
VERSION AW059842.1 GI:6652164  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 41)

REFERENCE  
AUTHORS Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,  
McCollum, C., Mao, J.I., Kirchner, J.J., Eletre, S., DuBridge, R.B.,  
Burcham, T. and Albrecht, G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

JOURNAL MEDLINE  
PUBMED 20144098  
COMMENT Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology.  
Collected from the up-regulated gate. Consensus sequence of 363  
sequences in cluster.  
High quality sequence stop: 41.  
Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/clone\_lib="UPC15"  
/notes="Vector: pCR2.1; Cloning of PCR products from  
micro-beads carrying 3' end of up-regulated cDNA. THP-1  
cells induced with 100 nM PMA in DMSO. "

FEATURES  
source

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
||  
Db 40 GY 41

RESULT 39  
AW059847/c  
LOCUS  
DEFINITION HuTh.best.upc15.final.cluster\_6 (24) UPC15 Homo sapiens cDNA  
similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.

ACCESSION AW059847  
VERSION AW059847.1 GI:6652169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 41)

REFERENCE  
AUTHORS Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,  
McCollum, C., Mao, J.I., Kirchner, J.J., Eletre, S., DuBridge, R.B.,  
Burcham, T. and Albrecht, G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

JOURNAL MEDLINE  
PUBMED 20144098  
COMMENT Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology.  
Collected from the up-regulated gate. Consensus sequence of 363  
sequences in cluster.  
High quality sequence stop: 41.  
Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="UPC15"  
/notes="Vector: pCR2.1; Cloning of PCR products from  
micro-beads carrying 3' end of up-regulated cDNA. THP-1  
cells induced with 100 nM PMA in DMSO. "

FEATURES  
source

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4  
||  
Db 28 RC 27

RESULT 37





ACCESSION AL059436.1 GI:4947000  
 VERSION AL059436.1  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
 source  
 Location/Qualifiers  
 1..43  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACR26P07"  
 /clone\_lib="RPCI-98"  
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ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 GY 8  
 ||  
 Db 38 GY 39

RESULT 42  
 CNS00COG/c  
 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26P07 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION AL059436  
 VERSION AL059436.1 GI:4947000  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
 source  
 Location/Qualifiers  
 1..43  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACR26P07"  
 /clone\_lib="RPCI-98"  
 /note="end : TET3"

ORIGIN  
 Query Match 20.0%; Score 2; DB 9; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 RC 4  
 ||  
 Db 39 RC 38

RESULT 43  
 CNS13621  
 LOCUS  
 DEFINITION Fg06\_02107 A Fg06\_AAFc ECORC Fusarium graminearum perithecia Gibberella zeae cDNA clone Fg06\_02107, mRNA sequence.  
 ACCESSION CNS13621  
 VERSION CNS13621.1 GI:47837632  
 KEYWORDS EST.  
 SOURCE Gibberella zeae (anamorph: Fusarium graminearum)  
 ORGANISM Gibberella zeae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreales; Nectriaceae; Gibberella.  
 REFERENCE 1 (bases 1 to 45)  
 AUTHORS Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J., Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.  
 TITLE Expressed Sequence Tags from Fusarium graminearum enriched for late stage perithecia  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Harris, Linda J.  
 Eastern Cereal and Oilseed Research Centre  
 Agriculture and Agri-food Canada  
 Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6, CANADA  
 Tel: (613) 759-1314  
 Fax: (613) 759-6566  
 Email: harrisl@agr.gc.ca.

FEATURES  
 source  
 Location/Qualifiers  
 1..45  
 /organism="Gibberella zeae"  
 /mol\_type="mRNA"  
 /strain="DAOM 180378"  
 /db\_xref="taxon:5518"  
 /clone="Fg06\_02107"  
 /dev\_stage="Sexual"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Fg06\_AAFc ECORC Fusarium graminearum perithecia"  
 /note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown on carrot agar at 20oC until confluent; perithecia induced with Tween 40 solution (25% v/v). Fruiting bodies were collected 20 days after induction. Total RNA was extracted using Trizol. cDNAs were amplified using Invitrogen GeneRacer kit. cDNA was not fractionated and was

```

ORIGIN
Query Match      20.0%; Score 2; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5
    ||
Db 11 CW 12

RESULT 44
CN813621/c
LOCUS
DEFINITION
Fg06_02107_A Fg06_AAFc_ECORC_Fusarium graminearum perithecia
Gibberella zeae cDNA clone Fg06_02107, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Gibberella zeae (anamorph: Fusarium graminearum)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocerales; Nectriaceae; Gibberella.
1 (bases 1 to 45)
Harris,L.J., Rocheleau,H., Quillet,T., Allard,S., Chapados,J.,
Couroux,P., De Moers,A., Hattori,J.I., Lacroix,C., Masotti,M.,
Robert,L.S., Singh,J.A., Spratt,D. and Linker,N.A.
Expressed Sequence Tags from Fusarium graminearum enriched for late
stage perithecia
Unpublished (2004)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrisjl@agr.gc.ca.

FEATURES
source
1..45
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg06_02107"
/dev_stage="Sexual"
/lab_host="F. coli DH10B"
/clone_lib="Fg06_AAFc_ECORC_Fusarium graminearum_peritheci
a"
/note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown
on carrot agar at 20°C until confluent; perithecia induced
with Tween 40 solution (25% v/v). Fruiting bodies were
collected 20 days after induction. Total RNA was extracted
using Trizol. cDNAs were amplified using Invitrogen
Genekacer Kit. cDNA was not fractionated and was
bidirectionally cloned."

ORIGIN
Query Match      20.0%; Score 2; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
    ||
Db 12 WG 11

RESULT 45
AW059540
LOCUS
DEFINITION
HUTH.bsst.dnc15.final.cluster_17 (10) DNC15 Homo sapiens cDNA
similar to catalase, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47)
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

FEATURES
source
1..47
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"
/note="Vector: pCR2.1; Cloning of PCR products from
micro-beads carrying 3' end of down-regulated cDNA. THP-1
cells non-induced (treated with DMSO only)."

ORIGIN
Query Match      20.0%; Score 2; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4
    ||
Db 1 RC 2

RESULT 46
AW059540/c
LOCUS
DEFINITION
HUTH.bsst.dnc15.final.cluster_17 (10) DNC15 Homo sapiens cDNA
similar to catalase, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47)
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

COMMENT
Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338

```

Fax: 510 670 9302  
 Email: timb@lynxgen.com  
 Sequence obtained from LYNX Therapeutics Megasort technology.  
 Collected from the down-regulated gate. Consensus sequence of 10  
 sequences in cluster.  
 High quality sequence stop: 47.

# FEATURES

Location/Qualifiers  
 1..47

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /note="Vector: PCR2.1; Cloning of PCR products from  
 micro-beads carrying 3' end of down-regulated cDNA. THP-1  
 cells non-induced (treated with DMSO only)."

# ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8  
 ||  
 Db 2 GY 1

# RESULT 47

CNS000J6U 48 bp DNA linear GSS 03-JUN-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:  
 DEFINITION BACR38C14 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.

ACCESSION AL075800

VERSION AL075800.1 GI:4955479

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 48)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

# FEATURES

Location/Qualifiers  
 1..48

/organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
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 /clone\_lib="BACR38C14"  
 /clone\_lib="RPCI-98"  
 /note="end : T7"

# ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8  
 ||  
 Db 35 GY 36

# RESULT 48

CNS000J6U/c

LOCUS Drosophila melanogaster

DEFINITION BACR38C14 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL075800

VERSION AL075800.1 GI:4955479

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 48)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES

Location/Qualifiers  
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/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

/clone\_lib="BACR38C14"

/clone\_lib="RPCI-98"

/note="end : T7"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4  
 ||  
 Db 36 RC 35

# RESULT 49

AW496816

LOCUS AW496816

DEFINITION 1Cj Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens

cDNA 3' similar to ubiquitin-protein ligase E3-alpha (UBR1), mRNA

sequence.

ACCESSION AW496816

VERSION AW496816.1 GI:7118839

KEYWORDS EST.

SOURCE Homo sapiens (human)

```

ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          Bevoit,M.
JOURNAL        Analysis of gene expression during neuronal differentiation of
COMMENT        NT2/D1 cells
                Unpublished (2000)
                Contact: Bevoit M
                Department of Growth and Reproduction GR-5064
                Copenhagen University Hospital
                Blegdamsvej 9, 2100 Copenhagen, Denmark
                Tel: +45 35455081
                Fax: +45 35456054
                Email: maja@biobase.dk
                The EST is up regulated, during neuronal differentiation of the
                NT2/D1 cell line (replated fully differentiated neurones not
                analysed).
PCR Primers    FORWARD: CCAATCCCGAGTT
                BACKWARD: AGCTTTTITTTTGG
                Seq primer: T7, CYS-TAATAGCACTCACTATAGGGCC
                High quality sequence stop: 49.
FEATURES       Location/Qualifiers
                1..49
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
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                /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                line."
                /note="The EST is derived from direct sequencing of a
                differential Display fragment. Laboratory manuals are
                available from http://www.biobase.dk/-ddbse"
ORIGIN
Query Match      20.0%; Score 2; DB 2; Length 49;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              6 WG 7
                ||
                3 WG 2
                ||
RESULT 51
LOCUS      CNS000AWB
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR22A09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL056017
VERSION     1
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 50)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segret@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoler in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES       Location/Qualifiers
                1..50
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                /mol_type="genomic DNA"
                /db_xref="taxon:7227"
                /clone="BACR22A09"
                /clone_lib="RPCI-98"
                /note="end : TET3"
ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 50;

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CY 8  
||  
Db 18 CY 19

RESULT 52  
CNS00AWB/c CNS00AWB 50 bp DNA linear GSS 04-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
DEFINITION BACR22A09 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL056017 GI:4936887

VERSION AL056017.1 GI:4936887

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 50)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mamoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
ECORI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source

1..50  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="BACR22A09"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4  
||  
Db 45 RC 44

RESULT 53  
AW444398 51 bp mRNA linear EST 25-SEP-2000  
LOCUS AB558 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA  
DEFINITION sequence.

ACCESSION AW444398

VERSION AW444398.1 GI:10282196

KEYWORDS EST.

SOURCE Agaricus bisporus

ORGANISM Agaricus bisporus

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Agaricales; Agaricaceae; Agaricus.

1 (bases 1 to 51)

AUTHORS Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.  
TITLE Classification of sequences expressed during the primordial and  
basidiome stages of the cultivated mushroom Agaricus bisporus  
Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL 20374017

MEDLINE 10919377

PUBMED

COMMENT Contact: Manuel D. Ospina-Giraldo  
Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University  
305 Buckhout, University Park, PA 16802, USA  
Tel: 8148633073  
Fax: 8148637217  
Email: mxoll@psu.edu

Seq primer: T7.

FEATURES  
source

Location/Qualifiers  
1..51

/organism="Agaricus bisporus"

/mol\_type="mRNA"

/strain="Sylvan-130"

/db\_xref="taxon:5341"

/tissue\_type="Primordium"

/clone\_lib="Primordium cDNA library"

/note="Vector: pBluescript II SK (+); Site\_1: SalI;

Site\_2: NotI"

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CY 8

||

Db 36 CY 37

RESULT 54

AW444398/c

LOCUS

DEFINITION

AB558 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA

sequence.

ACCESSION AW444398

VERSION AW444398.1 GI:10282196

KEYWORDS EST.

SOURCE Agaricus bisporus

ORGANISM Agaricus bisporus

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Agaricales; Agaricaceae; Agaricus.

1 (bases 1 to 51)

AUTHORS Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.  
TITLE Classification of sequences expressed during the primordial and  
basidiome stages of the cultivated mushroom Agaricus bisporus  
Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL 20374017

MEDLINE 10919377

PUBMED

COMMENT Contact: Manuel D. Ospina-Giraldo  
Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University  
305 Buckhout, University Park, PA 16802, USA  
Tel: 8148633073  
Fax: 8148637217  
Email: mxoll@psu.edu

Seq primer: T7.

FEATURES  
source

Location/Qualifiers  
1..51

/organism="Agaricus bisporus"

/mol\_type="mRNA"

/strain="Sylvan-130"

/db\_xref="taxon:5341"

/tissue\_type="Primordium"

/clone\_lib="Primordium cDNA library"

/note="Vector: pBluescript II SK (+); Site\_1: SalI;

ORIGIN	Site_2: NotI"	AL057009.1 GI:4937576	VERSION KEYWORDS SOURCE ORGANISM	GSS. Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 51) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
QY	3 RC 4 		REFERENCE AUTHORS TITLE JOURNAL	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> .
Db	37 RC 36		FEATURES source	Location/Qualifiers 1..51 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR23P07" /clone_lib="RPCI-98" /note="end : T7"
RESULT 55			ORIGIN	Query Match 20.0%; Score 2; DB 9; Length 51; Best Local Similarity 100.0%; Pred. No. 0; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CNS00BFG			QY	7 GY 8 
DEFINITION			Db	35 GY 34
ACCESSION			RESULT 57	
VERSION			CNS00IH3	
KEYWORDS			LOCUS	
SOURCE			DEFINITION	CNS00IH3 Drosophila melanogaster genome survey sequence TET3 end of BAC; BACR36D06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ORGANISM			ACCESSION	AL074772
REFERENCE			VERSION	AL074772.1 GI:4954552
AUTHORS			KEYWORDS	GSS.
TITLE			SOURCE	Drosophila melanogaster (fruit fly)
JOURNAL			ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 51) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT			REFERENCE AUTHORS TITLE JOURNAL	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> .
ORIGIN			COMMENT	
Query Match 20.0%; Score 2; DB 2; Length 51; Best Local Similarity 100.0%; Pred. No. 0; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	3 RC 4 			
Db	37 RC 36			
RESULT 55				
CNS00BFG				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

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1. .51
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36D06"
/clone_lib="RPCI-98"
/note="end : TET3"
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## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4

Db 36 RC 37

## RESULT 58

CNS001H3/c

## LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR36D06 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.

## ACCESSION

AL074772.1 GI:4954552

## VERSION

GSS.

## KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

## COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

```
1. .51
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36D06"
/clone_lib="RPCI-98"
/note="end : TET3"
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## ORIGIN

## Query Match

Best Local Similarity

Matches

Qy 7 QY 8

Db 37 QY 36

RESULT 59

CNS02CBU

## LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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REFERENCE

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JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE





Seq primer: T7, CYS-TAATACGACTCACTATAGGCCC  
High quality sequence stop: 52.

#### FEATURES

source  
1..52  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_lines="NT2/D1"  
/clone\_lib="Neuronal Differentiation of the NT2/D1 cell line."  
/note="The EST is derived from direct sequencing of a Differential Display fragment. Laboratory manuals are available from <http://www.biobase.dk/~ddbse>"

#### ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 WG 7  
||  
Db 23 WG 22

#### RESULT 63

CNS0102A 52 bp DNA linear GSS 26-JUL-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
DEFINITION BACN03D23 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL098428

#### ACCESSION

VERSION AL098428.1 GI:5610039

#### KEYWORDS

#### SOURCE

ORGANISM Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 52)

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

#### FEATURES

#### source

1..52  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN03D23"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#### Qy 3 RC 4

||

Db 30 RC 31

#### RESULT 64

#### CNS0102A/c

#### LOCUS

#### DEFINITION

AL098428

#### ACCESSION

VERSION AL098428.1 GI:5610039

#### KEYWORDS

#### SOURCE

#### ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 52)

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

#### FEATURES

#### source

1..52  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN03D23"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8

||

Db 31 GY 30

#### RESULT 65

#### CNS0110Z

#### LOCUS

#### DEFINITION

AL100541

#### ACCESSION

VERSION AL100541.1 GI:5612152

#### KEYWORDS

#### SOURCE

#### ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 52)

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector pBelobAC11.

#### FEATURES

source  
Location/Qualifiers  
1..52  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN06P24"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5  
||  
29 CW 30

#### RESULT 66

CNS0110Z/c

LOCUS

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN06P24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION AL100541.1 GI:5612152

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers  
1..52  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN06P24"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7  
||  
30 WG 29

#### RESULT 67

CNS011VR

LOCUS

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN06E01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC BACN06E01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION AL100785

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers  
1..52  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN06E01"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5  
||  
35 CW 36

#### RESULT 68

CNS011VR/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC BACN06E01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION AL100785

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

```

FEATURES
  source
    Location/Qualifiers
    1..52
      /organism="Drosophila melanogaster"
      /mol_type="genomic DNA"
      /db_xref="taxon:7227"
      /clone="BACN06E01"
      /clone_lib="DrosBAC"
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  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
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Db      3 CW 2

RESULT 69
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DEFINITION Aedes aegypti ASAP ID: 36043 unknown mRNA sequence.
ACCESSION AY432321
VERSION    AY432321.1 GI:42762493
KEYWORDS   HTC.
SOURCE     Aedes aegypti (yellow fever mosquito)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE  1 (bases 1 to 53)
            Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
            Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
            Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
            Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
            Christensen, B.M.
            Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
            Infect. Immun. 72 (7), 4114-4126 (2004)

REFERENCE  2 (bases 1 to 53)
            Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
            Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
            Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
            Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
            Christensen, B.M.
            Direct Submission
            Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
            More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.

FEATURES
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      /mol_type="mRNA"
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      hours post-inoculation"
      /db_xref="taxon:7159"
      /sex="female"
      /cell_type="hemocyte"
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  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
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Db      7 WG 6

RESULT 70
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LOCUS      AY432321
DEFINITION Aedes aegypti ASAP ID: 36043 unknown mRNA sequence.
ACCESSION AY432321
VERSION    AY432321.1 GI:42762493
KEYWORDS   HTC.
SOURCE     Aedes aegypti (yellow fever mosquito)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE  1 (bases 1 to 53)
            Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
            Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
            Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
            Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
            Christensen, B.M.
            Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
            Infect. Immun. 72 (7), 4114-4126 (2004)

REFERENCE  2 (bases 1 to 53)
            Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
            Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
            Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
            Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
            Christensen, B.M.
            Direct Submission
            Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
            More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.

FEATURES
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      /isolation_source="perfused hemolymph of
      bacteria-inoculated organisms at 1, 3, 6, 12, and 24
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      /db_xref="taxon:7159"
      /sex="female"
      /cell_type="hemocyte"
      /tissue_type="hemolymph"
      /dev_stage="adult"
      /note="ASAP-UW Feature ID: 36042"

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ORIGIN

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DEFINITION	AY440477					
ACCESSION	AY440477					
VERSION	AY440477.1	GI:42765506				
KEYWORDS	HTC					
SOURCE	Armigeres subalbatus					
ORGANISM	Armigeres subalbatus					
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Armigeres.					
AUTHORS	1 (bases 1 to 53)					
	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Ruch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.					
TITLE	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus					
JOURNAL	Infect. Immun. 72 (7), 4114-4126 (2004)					
PUBMED	15213157					
REFERENCE	2 (bases 1 to 53)					
AUTHORS	Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Ruch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao					



ACCESSION	VERSION	sapiens
AW49762		AW49762
		AW49762

**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
**AUTHORS** Bevolt, M.  
**TITLE** Analysis of gene expression during neuronal differentiation of NT2/D1 cells  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Bevolt M  
 Department of Growth and Reproduction GR-5064  
 Copenhagen University Hospital  
 Blegdamsvej 9, 2100 Copenhagen, Denmark  
 Tel: +45 35455081  
 Fax: +45 35456054  
 Email: majja@biobase.dk  
 The EST's expression level is constant, during neuronal differentiation of the NT2/D1 cell line.

**FEATURES**  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /cell\_lines="NT2/D1"  
 /clone\_lib="Neuronal Differentiation of the NT2/D1 cell line."  
 /note="The EST is derived from direct sequencing of a Differential Display fragment. Laboratory manuals are available from <http://www.biobase.dk/~ddbse>"

**ORIGIN**  
 Query Match 20.0%; Score 2; DB 2; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CW 5  
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 Db 18 CW 17

**RESULT 79**  
**CNS025NE** 55 bp DNA linear GSS 01-SEP-2000  
**LOCUS** Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
**DEFINITION** 238C04 of library G from Tetraodon nigroviridis, genomic survey sequence.

**ACCESSION** AL182291  
**VERSION** AL182291.1 GI:7820389  
**KEYWORDS** GSS; genome survey sequence.  
**SOURCE** Tetraodon nigroviridis  
**ORGANISM** Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

**REFERENCE**  
**AUTHORS** 1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)  
**MEDLINE** 20296633  
**PUBMED** 10835645

**REFERENCE**  
**AUTHORS** 2 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)  
**MEDLINE** 20296633  
**PUBMED** 10835645

**REFERENCE**  
**AUTHORS** 3 (bases 1 to 55)  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)  
**MEDLINE** 20359837  
**PUBMED** 10899143

**TITLE** Saurin, W., Bernot, A. and Weissenbach, J.  
**JOURNAL** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
**MEDLINE** Genome Res. 10 (7), 939-949 (2000)  
**PUBMED** 20359837  
**REFERENCE** 10899143  
**AUTHORS** 3 (bases 1 to 55)  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
**COMMENT** - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

**FEATURES**  
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**ORIGIN**  
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**RESULT 80**  
**CNS025NE** 55 bp DNA linear GSS 01-SEP-2000  
**LOCUS** Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
**DEFINITION** 238C04 of library G from Tetraodon nigroviridis, genomic survey sequence.

**ACCESSION** AL182291  
**VERSION** AL182291.1 GI:7820389  
**KEYWORDS** GSS; genome survey sequence.  
**SOURCE** Tetraodon nigroviridis  
**ORGANISM** Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

**REFERENCE**  
**AUTHORS** 1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)  
**MEDLINE** 20296633  
**PUBMED** 10835645

**REFERENCE**  
**AUTHORS** 2 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)  
**MEDLINE** 20359837  
**PUBMED** 10899143

**REFERENCE**  
**AUTHORS** 3 (bases 1 to 55)  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 This sequence is a single read and was generated as part of a large  
 scale clone-end sequencing project of the Tetraodon nigroviridis  
 genome. For more information, please take a look at  
 http://www.genoscope.cns.fr/Tetraodon.

# FEATURES

1. .55  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone\_lib="238C04"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : C0AG238BB02SP1-end :  
 PUC-Ori"

## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CY 8  
 Db 34 GY 33

## RESULT 81

AW444238  
 LOCUS  
 DEFINITION  
 AB562 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA  
 EST.  
 ACCESSION  
 AW444238  
 VERSION  
 AW444238.1 GI:10282036  
 KEYWORDS  
 EST.  
 SOURCE  
 Agaricus bisporus  
 ORGANISM  
 Agaricus bisporus  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Agaricales; Agaricaceae; Agaricus.  
 REFERENCE  
 1 (bases 1 to 56)  
 AUTHORS  
 Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.  
 TITLE  
 Classification of sequences expressed during the primordial and  
 basidiome stages of the cultivated mushroom Agaricus bisporus  
 JOURNAL  
 Fungal Genet. Biol. 29 (2), 81-94 (2000)  
 MEDLINE  
 20374017  
 PUBMED  
 10919377  
 COMMENT  
 Contact: Manuel D. Ospina-Giraldo  
 Mushroom Research Laboratory, Department of Plant Pathology  
 The Pennsylvania State University  
 305 Buckhout, University Park, PA 16802, USA  
 Tel: 8148633073  
 Fax: 8148637217  
 Email: mxoll@psu.edu  
 Seq primer: T7.

# FEATURES

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 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="Sylvan-130"  
 /db\_xref="taxon:5341"  
 /tissue\_type="Basidiome"  
 /clone\_lib="Basidiome cDNA library"  
 /note="Vector: pBluescript II SK (+); Site\_1: SalI;  
 Site\_2: NotI"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7  
 Db 11 WG 12

## RESULT 82

AW444238/c  
 LOCUS  
 DEFINITION  
 AB562 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA  
 sequence.  
 ACCESSION  
 AW444238  
 VERSION  
 AW444238.1 GI:10282036  
 KEYWORDS  
 EST.  
 SOURCE  
 Agaricus bisporus  
 ORGANISM  
 Agaricus bisporus  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Agaricales; Agaricaceae; Agaricus.  
 REFERENCE  
 1 (bases 1 to 56)  
 AUTHORS  
 Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.  
 TITLE  
 Classification of sequences expressed during the primordial and  
 basidiome stages of the cultivated mushroom Agaricus bisporus  
 JOURNAL  
 Fungal Genet. Biol. 29 (2), 81-94 (2000)  
 MEDLINE  
 20374017  
 PUBMED  
 10919377  
 COMMENT  
 Contact: Manuel D. Ospina-Giraldo  
 Mushroom Research Laboratory, Department of Plant Pathology  
 The Pennsylvania State University  
 305 Buckhout, University Park, PA 16802, USA  
 Tel: 8148633073  
 Fax: 8148637217  
 Email: mxoll@psu.edu  
 Seq primer: T7.

# FEATURES

1. .56  
 Location/Qualifiers  
 /organism="Agaricus bisporus"  
 /mol\_type="mRNA"  
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 /tissue\_type="Basidiome"  
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 Site\_2: NotI"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5  
 Db 12 CW 11

## RESULT 83

AW444409  
 LOCUS  
 DEFINITION  
 AB573 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA  
 sequence.  
 ACCESSION  
 AW444409  
 VERSION  
 AW444409.1 GI:10282207  
 KEYWORDS  
 EST.  
 SOURCE  
 Agaricus bisporus  
 ORGANISM  
 Agaricus bisporus  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Agaricales; Agaricaceae; Agaricus.  
 REFERENCE  
 1 (bases 1 to 56)  
 AUTHORS  
 Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.  
 TITLE  
 Classification of sequences expressed during the primordial and  
 basidiome stages of the cultivated mushroom Agaricus bisporus  
 JOURNAL  
 Fungal Genet. Biol. 29 (2), 81-94 (2000)  
 MEDLINE  
 20374017  
 PUBMED  
 10919377  
 COMMENT  
 Contact: Manuel D. Ospina-Giraldo  
 Mushroom Research Laboratory, Department of Plant Pathology  
 The Pennsylvania State University  
 305 Buckhout, University Park, PA 16802, USA  
 Tel: 8148633073



```

Fax: 8148637217
Email: mxo11@psu.edu
Seq primer: T7.
FEATURES
    source
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                /mol_type="mRNA"
                /strain="Sylvan-130"
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                /note="Vector: pBluescript II SK (+); Site_1: SalI;
                Site_2: NotI"
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    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 WG 7
      ||
Db      24 WG 25

RESULT 84
AW444409/c
LOCUS
DEFINITION
    AS573 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
sequence.
ACCESSION
    AW444409
VERSION
    AW444409.1 GI:10282207
KEYWORDS
    EST.
SOURCE
    ORGANISM
        Agaricus bisporus
        Agaricus bisporus
        Eukaryota; Fungi; Basidiomycetes; Hymenomycetes; Homobasidiomycetes;
        Agaricales; Agaricaceae; Agaricus.
REFERENCE
    1 (bases 1 to 56)
AUTHORS
    Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
TITLE
    Classification of sequences expressed during the primordial and
    basidiome stages of the cultivated mushroom Agaricus bisporus
JOURNAL
    Fungal Genet. Biol. 29 (2), 81-94 (2000)
MEDLINE
    20374017
PUBMED
    10919377
COMMENT
    Contact: Manuel D. Ospina-Giraldo
    Mushroom Research Laboratory, Department of Plant Pathology
    The Pennsylvania State University
    305 Buckhout, University Park, PA 16802, USA
    Tel: 8148633073
    Fax: 8148637217
    Email: mxo11@psu.edu
    Seq primer: T7.
FEATURES
    source
        Location/Qualifiers
            1..56
                /organism="Agaricus bisporus"
                /mol_type="mRNA"
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                /note="Vector: pBluescript II SK (+); Site_1: SalI;
                Site_2: NotI"
ORIGIN
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    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 CW 5
      ||
Db      25 CW 24

RESULT 85

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BG838323
LOCUS
DEFINITION
    Gc01_08e06 R Gc01_AAPC_ECORC cold stressed Glycine clandestina
    Glycine clandestina cDNA clone Gc01_08e06, mRNA sequence.
ACCESSION
    BG838323
VERSION
    BG838323.1 GI:14204645
KEYWORDS
    EST.
SOURCE
    ORGANISM
        Glycine clandestina
        Glycine clandestina
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
        Glycine.
REFERENCE
    1 (bases 1 to 56)
AUTHORS
    Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
    Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
    Tinker,N.A.
TITLE
    Expressed Sequence Tags from Cold-Stressed Glycine clandestina
    Seedlings
JOURNAL
    Unpublished (2001)
COMMENT
    Contact: Singh,J.A.
    Eastern Cereal and Oilseed Research Centre
    Agriculture and Agri-food Canada
    KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
    OC6, Canada
    Tel: (613) 759-1662
    Fax: (613) 759-1701
    Email: singhja@agr.gc.ca.
FEATURES
    source
        Location/Qualifiers
            1..56
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                /mol_type="mRNA"
                /cultivar="1035"
                /db_xref="taxon:45687"
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                ina"
                /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
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                of light/day. Harvested after only 2-3 days of cold
                treatment. cDNA was prepared with the Uni-zap cDNA kit
                from Stratagene. Eco RI adapters were linked followed by
                digest with Xho I/Eco RI and ligated to pBluescript."
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      7 GY 8
      ||
Db      43 GY 44

RESULT 86
BG838323/c
LOCUS
DEFINITION
    Gc01_08e06 R Gc01_AAPC_ECORC cold stressed Glycine clandestina
    Glycine clandestina cDNA clone Gc01_08e06, mRNA sequence.
ACCESSION
    BG838323
VERSION
    BG838323.1 GI:14204645
KEYWORDS
    EST.
SOURCE
    ORGANISM
        Glycine clandestina
        Glycine clandestina
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
        Glycine.
REFERENCE
    1 (bases 1 to 56)
AUTHORS
    Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
    Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
    Tinker,N.A.

```

**TITLE** Expressed Sequence Tags from Cold-Stressed Glycine clandestina  
**JOURNAL** Seedlings  
**COMMENT** Unpublished (2001)  
 Contact: Singh, J.A.  
 Eastern Cereal and Oilseed Research Centre  
 Agriculture and Agri-food Canada  
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A  
 0C6, Canada  
 Tel: (613) 759-1662  
 Fax: (613) 759-1701  
 Email: singhja@agr.gc.ca.

**FEATURES**  
 source  
 1. .56  
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 /organism="Glycine clandestina"  
 /mol\_type="mRNA"  
 /cultivar="1035"  
 /db\_xref="taxon:45687"  
 /clone="Gc01\_08e06"  
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 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pBluescript.c."

**ORIGIN**

Query Match 20.0%; Score 2; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4  
 ||  
 Db 44 RC 43

**RESULT 87**  
**CNS013GI**  
**LOCUS** CNS013GI 56 bp DNA linear GSS 26-JUL-1999  
**DEFINITION** Drosophila melanogaster genome survey sequence T7 end of BAC BACN10D06 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
**ACCESSION** AL102828  
**VERSION** AL102828.1 GI:5614439  
**KEYWORDS** GSS.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

**REFERENCE**  
**AUTHORS** 1. (bases 1 to 56)  
**TITLE** Genoscope.  
**JOURNAL** Direct Submission  
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
**COMMENT** Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

**FEATURES**  
source

1. .56  
 Location/Qualifiers  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACN10D06"  
 /clone\_lib="DrosBAC"

**ORIGIN**

Query Match 20.0%; Score 2; DB 9; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 RC 4  
 ||  
 Db 50 RC 51

**RESULT 88**  
**CNS013GI/c**  
**LOCUS** CNS013GI 56 bp DNA linear GSS 26-JUL-1999  
**DEFINITION** Drosophila melanogaster genome survey sequence T7 end of BAC BACN10D06 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
**ACCESSION** AL102828  
**VERSION** AL102828.1 GI:5614439  
**KEYWORDS** GSS.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

**REFERENCE**  
AUTHORS

Direct Submission  
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
**COMMENT** Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

**FEATURES**

source  
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 Location/Qualifiers  
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**ORIGIN**

Query Match 20.0%; Score 2; DB 9; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8  
 ||  
 Db 51 GY 50

**RESULT 89**

**CNS00BH8**  
**LOCUS** CNS00BH8 57 bp DNA linear GSS 04-JUN-1999  
**DEFINITION** Drosophila melanogaster genome survey sequence T7 end of BAC # BACR23G24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
**ACCESSION** AL057073  
**VERSION** AL057073.1 GI:4937640  
**KEYWORDS** GSS.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 57)

## AUTHORS

Genoscope.

## TITLE

Direct Submission

## JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

## COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

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## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 57;  
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7

Db 49 WG 50

## RESULT 90

CNS000BH8/c

## LOCUS

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR23G24 of RPCL-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## ACCESSION

AL057073.1 GI:4937640

## VERSION

GSS.

## KEYWORDS

SOURCE Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 57)

## REFERENCE

AUTHORS

## TITLE

Direct Submission

## JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

## COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

Db 50 CW 49

## RESULT 91

CNS0217V

## LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 224P22 of library G from Tetraodon nigroviridis, genomic survey sequence.

## ACCESSION

AL176548

## VERSION

GI:7814605

## KEYWORDS

GSS; genome survey sequence.

## SOURCE

ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

## REFERENCE

AUTHORS

Roest Crolius H., Jaillon O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fizames C., Wincker P., Brottier P., Quetier F., Saurin W. and Weissbach J.  
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

## TITLE

JOURNAL

MEDLINE

PUBMED

20296633

10835645

2

AUTHORS

Roest Crolius H., Jaillon O., Dasilva C., Ozouf-Costaz C., Fizames C., Fischer C., Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and Weissbach J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

10899143

3 (bases 1 to 57)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr))

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

<http://www.genoscope.cns.fr/tetraodon>.

Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:99883"

/clone="224P22"

/clone\_lib="G"



ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE 1  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645

REFERENCE 2  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10899143

REFERENCE 3 (bases 1 to 57)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

FEATURES  
source Location/Qualifiers  
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/clone\_lib="G"  
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GY 8  
||  
Db 49 GY 48

RESULT 95  
CNS03R92  
LOCUS  
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
049119 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL256943  
VERSION AL256943.1 GI:7977955  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE 1  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645

REFERENCE 2  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10899143

REFERENCE 3 (bases 1 to 57)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

FEATURES  
source Location/Qualifiers  
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/clone="049119"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0BG049AE10SP1-end :  
PUC-Ori"

ORIGIN  
Query Match 20.0%; Score 2; DB 9; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 WG 7  
||  
Db 51 WG 52

RESULT 96  
CNS03R92/c  
LOCUS  
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
049119 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL256943  
VERSION AL256943.1 GI:7977955  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE 1  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645

REFERENCE 2  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

[illegible]



```

FEATURES
source
Location/Qualifiers
1..59
/organism="Armigeres subalbatus"
/mol_type="mRNA"
/isolation_source="perfused hemolymph of
bacteria-innoculated organisms at 1, 3, 6, 12, and 24
hours post-inoculation"
/db_xref="taxon:124917"
/sex="female"
/cell_type="hemocyte"
/tissue_type="hemolymph"
/dev_stage="adult"
/notes="ASAP-UW Feature ID: 42100"

misc_feature
1..59
/notes="unknown; low quality sequence; ASAP-UW Feature ID:
42101"

ORIGIN
Query Match 20.0%; Score 2; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 41 CW 42

RESULT 102
AV439538/c
LOCUS
DEFINITION
Armigeres subalbatus ASAP ID: 42101 unknown mRNA sequence.
ACCESSION
AV439538
VERSION
AY439538.1 GI:42764563
KEYWORDS
HTC.
SOURCE
Armigeres subalbatus
ORGANISM
Armigeres subalbatus
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Armigeres.
1 (bases 1 to 59)
Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
Fuchs, J.P., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
Christensen, B.M.
Description of the Transcriptomes of Immune Response-Activated
Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
subalbatus
Infect. Immun. 72 (7), 4114-4126 (2004)
15213157
2 (bases 1 to 59)
Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
Liss, P., Rusch, M., Fuchs, J.P., Butler, K.M., Wu, R.C.-C., Kuo, H.-K.,
Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C.,
Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.
Direct Submission
Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
53706, USA
More information about this sequence is available in ASAP (A
Systematic Annotation Package for community analysis of genomes)
from the University of Wisconsin-Madison at
https://asap.ahabs.wisc.edu/annotation/php/lookup.php.
Location/Qualifiers
1..59
/organism="Armigeres subalbatus"
/mol_type="mRNA"
/isolation_source="perfused hemolymph of
bacteria-innoculated organisms at 1, 3, 6, 12, and 24
hours post-inoculation"
/db_xref="taxon:124917"
/sex="female"
/cell_type="hemocyte"

FEATURES
source
Location/Qualifiers
1..59
/organism="Armigeres subalbatus"
/mol_type="mRNA"
/db_xref="taxon:124917"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 104
CNS0111A/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099688
VERSION
AL099688.1 GI:5611299
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.
Location/Qualifiers
1..59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 104
CNS0111A/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099688
VERSION
AL099688.1 GI:5611299
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.
Location/Qualifiers
1..59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 103
CNS0111A
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099688
VERSION
AL099688.1 GI:5611299
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.
Location/Qualifiers
1..59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 103
CNS0111A
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099688
VERSION
AL099688.1 GI:5611299
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.
Location/Qualifiers
1..59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 103
CNS0111A
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099688
VERSION
AL099688.1 GI:5611299
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.
Location/Qualifiers
1..59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/notes="end : SP6"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
||
Db 43 RR 44

RESULT 103
CNS0111A
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
```



KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 59)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES  
source  
1..59  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN05J19"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : SP6"

## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 59;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 9

||

Db 44 YY 43

## RESULT 105

CNS0141M  
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
DEFINITION BACN11G20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL104200.1 GI:5615811  
VERSION  
KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

## FEATURES

source

1..59  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"

## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 59;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 6

||

Db 56 WW 57

## RESULT 106

CNS0141M  
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
DEFINITION BACN11G20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL104200.1 GI:5615811  
VERSION  
KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

## FEATURES

source

1..59  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN11G20"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : SP6"

## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 59;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 6

||

Db 57 WW 56

## RESULT 107

AW059629  
LOCUS HUTH.bsst.dnc15.final.cluster.119 (2) DNC15 Homo sapiens cDNA  
DEFINITION similar to KIAA0741, mRNA sequence.  
ACCESSION AW059629.1 GI:6651951  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 60)  
Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K., McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B., Burcham, T. and Albrecht, G.  
TITLE  
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
MEDLINE  
20144098  
PUBMED  
10677516  
COMMENT  
Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate. Consensus sequence of 2 sequences in cluster.  
High quality sequence stop: 60.

FEATURES  
source  
Location/Qualifiers  
1..60  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"  
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4  
||  
Db 17 RC 18

RESULT 108  
AW059629/c  
LOCUS  
DEFINITION  
HUTH.best.dnc15.final.cluster\_119\_(2) DNC15 Homo sapiens cDNA similar to KIAA0741, mRNA sequence.  
ACCESSION  
AW059629  
VERSION  
AW059629.1 GI:6651951  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 60)  
Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K., McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B., Burcham, T. and Albrecht, G.

TITLE  
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
MEDLINE  
20144098  
PUBMED  
10677516

COMMENT  
Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate. Consensus sequence of 2 sequences in cluster.

FEATURES  
source  
Location/Qualifiers  
1..60  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"  
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
||  
Db 18 GY 17

RESULT 109  
AW582843

LOCUS  
DEFINITION  
top3966 Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens cDNA 3' similar to EST, mRNA sequence.  
ACCESSION  
AW582843  
VERSION  
AW582843.1 GI:7382089  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 60)  
Brevort, M.

REFERENCE  
AUTHORS  
TITLE  
Analysis of gene expression during neuronal differentiation of NT2/D1 cells  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Brevort M  
Department of Growth and Reproduction GR-5064  
Copenhagen University Hospital  
Blegdamsvej 9, 2100 Copenhagen, Denmark  
Tel: +45 35455081  
Fax: +45 35456054  
Email: maj@biobase.dk

The EST's expression level is constant, during neuronal differentiation of the NT2/D1 cell line (replated fully differentiated neurones not analysed).  
PCR Primers  
FORWARD: GGCCTTCCTGTGT  
BACKWARD: AAGCTTTTCTTTTTC  
Seq primer: T7, CV5-TAATACGACTCACTATAGGCGC  
High quality sequence stop: 60.

FEATURES  
source  
Location/Qualifiers  
1..60  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="NT2/D1"  
/clone\_lib="Neuronal Differentiation of the NT2/D1 cell line."  
/note="The EST is derived from direct sequencing of a differential display fragment. Laboratory manuals are available from <http://www.biobase.dk/-ddbase>"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2



